

SEARCH REQUEST FORM

Requestor's
Name:

Liu S

Serial
Number:

101757745

Date:

03-15-06

Phone:

Art Unit:

1653

REM 3A64/3C70

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Seq ID 2 : 115-121
54-140
145-153

EST dB 1000 Summary Listing
200 hits displayed

Extended Search

STAFF USE ONLY

Date completed:

Searcher:

Beverly e2528

Terminal time:

Elapsed time:

CPU time:

Total time:

Number of Searches:

Number of Databases:

Search Site

☐ STIC

☐ CM-1

☐ Pre-S

Type of Search

☐ N.A. Sequence

☐ A.A. Sequence

☐ Structure

☐ Bibliographic

Vendors

☐ IG

☐ STN

☐ Dialog

☐ APS

☐ Geninfo

☐ SDC

☐ DARC/Questel

☒ Other CGN

Thu Mar 16 10:39:26 2006

US-10-757-745-2_copy_145_153.rst

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 16, 2006, 00:29:49 ; Search time 706.806 Seconds

(without alignments)
595.756 Million cell updates/sec

Title: US-10-757-745-2_COPY_145_153

Profile score: 45

Sequence: 1 FDVFLQEV 9

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delep 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-O=/abs/ABSGMEM.spool/US1075745/runat.15032006.165652.3610/app.query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPTCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human0.cct -LIST=1000
-DOCALIGN=200 -THR.SCOR=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=200 -MODE=LOCAL
-OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USER=US1075745 @CN 1.8148 @runat.15032006.165652.3610 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*
10: gb_esc10:*
11: gb_esc11:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	159	3	BQ336306 PM1-MT014
2	45	100.0	146	3	BQ331200 MR4-ET014
3	45	100.0	247	2	BF768814 PM0-IT001
4	45	100.0	252	1	AA325145 EST28102
5	45	100.0	296	2	BF992136 OV3-GN020
6	45	100.0	313	2	BF992133 OV3-GN020
7	45	100.0	368	2	BE694706 PM0-BT075

8	45	100.0	388	1	AV659558	AV659558
9	45	100.0	394	1	AV661333	AV661333
10	45	100.0	413	3	BQ332322	BQ332322
11	45	100.0	419	2	BF853399	BF853399
12	45	100.0	422	2	BQ982044	BQ982044
13	45	100.0	429	5	BQ582059	BQ582059
14	45	100.0	435	3	BQ332331	BQ332331
15	45	100.0	437	2	BF768820	BF768820
16	45	100.0	440	2	BQ982029	BQ982029
17	45	100.0	440	2	BQ982036	BQ982036
18	45	100.0	441	2	BF692415	BF692415
19	45	100.0	441	2	BF693925	BF693925
20	45	100.0	444	2	BF693187	BF693187
21	45	100.0	447	2	BF691509	BF691509
22	45	100.0	453	2	BF773259	BF773259
23	45	100.0	453	3	BQ115535	BQ115535
24	45	100.0	454	2	BQ982031	BQ982031
25	45	100.0	456	2	BF996980	BF996980
26	45	100.0	456	3	BQ332321	BQ332321
27	45	100.0	458	3	BQ366782	BQ366782
28	45	100.0	459	2	BQ982034	BQ982034
29	45	100.0	460	2	BF693150	BF693150
30	45	100.0	461	2	BQ982012	BQ982012
31	45	100.0	463	2	BF652284	BF652284
32	45	100.0	463	2	BF652788	BF652788
33	45	100.0	463	2	BF693119	BF693119
34	45	100.0	471	2	BF693924	BF693924
35	45	100.0	471	7	CR543841	CR543841
36	45	100.0	473	6	CB120234	CB120234
37	45	100.0	480	1	AT750554	AT750554
38	45	100.0	485	1	AA486032	AA486032
39	45	100.0	491	1	AJ681912	AJ681912
40	45	100.0	491	2	B1016235	B1016235
41	45	100.0	530	3	BM46221	BM46221
42	45	100.0	534	7	CN289821	CN289821
43	45	100.0	546	2	BQ541031	BQ541031
44	45	100.0	549	1	AM669835	AM669835
45	45	100.0	554	3	BP220985	BP220985
46	45	100.0	565	3	BP226620	BP226620
47	45	100.0	566	3	BP226508	BP226508
48	45	100.0	568	3	BP257211	BP257211
49	45	100.0	570	3	BM172060	BM172060
50	45	100.0	570	3	BP221518	BP221518
51	45	100.0	570	3	BP258309	BP258309
52	45	100.0	572	3	BP262485	BP262485
53	45	100.0	573	1	AU279894	AU279894
54	45	100.0	573	3	BP221260	BP221260
55	45	100.0	573	3	BP261500	BP261500
56	45	100.0	576	3	BP262542	BP262542
57	45	100.0	577	7	CN298919	CN298919
58	45	100.0	580	3	BP261787	BP261787
59	45	100.0	580	3	BP274368	BP274368
60	45	100.0	581	1	AV1717253	AV1717253
61	45	100.0	581	3	BP207751	BP207751
62	45	100.0	581	3	BP225088	BP225088
63	45	100.0	581	3	BP262101	BP262101
64	45	100.0	581	3	BP262638	BP262638
65	45	100.0	581	3	BP270744	BP270744
66	45	100.0	581	3	BP349936	BP349936
67	45	100.0	581	3	BP379659	BP379659
68	45	100.0	581	6	CB286391	CB286391
69	45	100.0	582	3	BM507091	BM507091
70	45	100.0	582	3	BP219740	BP219740
71	45	100.0	582	3	BP233592	BP233592
72	45	100.0	582	3	BP234218	BP234218
73	45	100.0	582	3	BP261141	BP261141
74	45	100.0	582	3	BP261789	BP261789
75	45	100.0	582	3	BP263516	BP263516
76	45	100.0	582	3	BP270415	BP270415
77	45	100.0	582	3	BP275810	BP275810
78	45	100.0	583	3	BP195721	BP195721
79	45	100.0	583	3	BP262103	BP262103
80	45	100.0	583	3	BP262741	BP262741

81	45	100.0	583	3	BP19548	BP19548	BP19548	154	45	100.0	1087	7	CN643527	ILLUMIGEN
82	45	100.0	583	3	BP783329	BP783329	BP783329	155	45	100.0	1089	11	DD049205	Homo sapi
82	45	100.0	584	3	BP263059	BP263059	BP263059	156	45	100.0	1089	11	DD049206	Pan trogl
82	45	100.0	584	3	BP348623	BP348623	BP348623	157	45	100.0	1090	7	CN641671	ILLUMIGEN
82	45	100.0	584	3	BP236074	BP236074	BP236074	158	45	100.0	1100	3	BMS55041	AGENCOURT
82	45	100.0	588	3	BP348796	BP348796	BP348796	159	45	100.0	1103	3	CN601303	AGENCOURT
87	45	100.0	602	1	AL703449	DKR2P686G	AL703449	160	45	100.0	1103	3	CN601303	AGENCOURT
87	45	100.0	602	1	CB069952	1a31a1e10.y	CB069952	161	45	100.0	1103	3	CN601303	AGENCOURT
88	45	100.0	621	6	CB069952	1a31a1e10.y	CB069952	162	45	100.0	1103	3	CN601303	AGENCOURT
89	45	100.0	626	2	BP779791	602148451	BP779791	163	45	100.0	1103	3	CN601303	AGENCOURT
90	45	100.0	634	6	CB157906	K-EST0217	CB157906	164	45	100.0	1103	3	CN601303	AGENCOURT
91	45	100.0	634	7	CB023369	288.Fu11	CB023369	165	45	100.0	1103	3	CN601303	AGENCOURT
92	45	100.0	644	3	BP338830	602999333	BP338830	166	45	100.0	1103	3	CN601303	AGENCOURT
93	45	100.0	644	6	CP764797	CES0003181	CP764797	167	45	100.0	1103	3	CN601303	AGENCOURT
94	45	100.0	650	2	BQ431303	602499879	BQ431303	168	45	100.0	1103	3	CN601303	AGENCOURT
94	45	100.0	657	7	CN2898920	170006001	CN2898920	169	45	100.0	1103	3	CN601303	AGENCOURT
95	45	100.0	674	7	CN791432	4126155.B	CN791432	170	45	100.0	1103	3	CN601303	AGENCOURT
96	45	100.0	678	2	BP719113	602699045	BP719113	171	45	100.0	1103	3	CN601303	AGENCOURT
97	45	100.0	680	7	CP952220	4091710.B	CP952220	172	45	100.0	1103	3	CN601303	AGENCOURT
98	45	100.0	683	7	CN789157	4123581.B	CN789157	173	45	100.0	1103	3	CN601303	AGENCOURT
99	45	100.0	685	7	CP961492	411401.B	CP961492	174	45	100.0	1103	3	CN601303	AGENCOURT
100	45	100.0	701	7	CP767236	DKR2P469E	CP767236	175	45	100.0	1103	3	CN601303	AGENCOURT
101	45	100.0	710	5	BP661472	602998939	BP661472	176	45	100.0	1103	3	CN601303	AGENCOURT
102	45	100.0	710	5	BP661472	602998939	BP661472	177	45	100.0	1103	3	CN601303	AGENCOURT
103	45	100.0	710	5	BP661472	602998939	BP661472	178	45	100.0	1103	3	CN601303	AGENCOURT
104	45	100.0	711	7	CN2898923	170006000	CN2898923	179	45	100.0	1103	3	CN601303	AGENCOURT
105	45	100.0	721	7	CN2898923	170006000	CN2898923	180	45	100.0	1103	3	CN601303	AGENCOURT
106	45	100.0	721	7	CN2898923	170006000	CN2898923	181	45	100.0	1103	3	CN601303	AGENCOURT
107	45	100.0	721	7	CN2898923	170006000	CN2898923	182	45	100.0	1103	3	CN601303	AGENCOURT
108	45</													

C 227	44	97.8	847	8	DB667246	JGI_CAB9	C 300	39	86.7	478	3	BP702326
C 228	44	97.8	850	6	CF378639	AGENCOURT	C 301	39	86.7	509	2	B0868432
C 229	44	97.8	860	8	CA958090	UGI_CAO9	C 302	39	86.7	579	2	BE997052
C 230	44	97.8	866	8	CK843565	UGI_CAK1	C 303	39	86.7	612	1	AI532142
C 231	44	97.8	876	7	CK798287	AGENCOURT	C 304	39	86.7	625	1	CB190354
C 232	44	97.8	879	8	CK797649	AGENCOURT	C 305	39	86.7	632	7	CK974856
C 233	44	97.8	879	8	CK824886	JGI_CAK4	C 306	39	86.7	636	5	BY717884
C 234	44	97.8	891	1	AI879624	AL879624	C 307	39	86.7	677	10	BX157554
C 235	44	97.8	894	5	BK776016	BK776016	C 308	39	86.7	743	10	AG015268
C 236	44	97.8	896	6	CA971409	AGENCOURT	C 309	39	86.7	751	10	AG015292
C 237	44	97.8	900	6	CA980929	AGENCOURT	C 310	39	86.7	754	10	AG015267
C 238	44	97.8	905	6	BK780455	BK780455	C 311	39	86.7	789	5	BX885044
C 239	44	97.8	909	6	CA982823	AGENCOURT	C 312	39	86.7	805	10	BX153274
C 240	44	97.8	919	6	CA973896	AGENCOURT	C 313	39	86.7	811	5	B0907830
C 241	44	97.8	927	6	CA972288	AGENCOURT	C 314	39	86.7	885	10	CNS01437
C 242	44	97.8	927	6	CA972607	AGENCOURT	C 315	38	84.4	347	5	BW590472
C 243	44	97.8	942	2	BG298330	AGENCOURT	C 316	38	84.4	371	8	DN134037
C 244	44	97.8	946	5	BU468774	BG298330	C 317	38	84.4	375	1	AD562626
C 245	44	97.8	961	2	BI150788	BI150788	C 318	38	84.4	405	10	CL450896
C 246	44	97.8	963	2	BI656151	BI656151	C 319	38	84.4	464	7	CV395524
C 247	44	97.8	984	5	BK846715	BK846715	C 320	38	84.4	504	7	CV395537
C 248	44	97.8	1077	5	BU131072	BU131072	C 321	38	84.4	544	7	BW576902
C 249	44	97.8	1289	4	AK009089	Mus_muscu	C 322	38	84.4	509	10	CG890558
C 250	42	93.3	467	3	BQ329405	MK3-EN008	C 323	38	84.4	515	5	BG533034
C 251	42	93.3	523	7	CK993108	019B07R1	C 324	38	84.4	532	7	CK689578
C 252	42	93.3	532	6	CB387482	CB387482	C 325	38	84.4	532	10	BX652342
C 253	42	93.3	544	3	BQ142674	BQ142674	C 326	38	84.4	537	6	CF341430
C 254	42	93.3	711	8	DE407274	36_Metcarh	C 327	38	84.4	559	3	BT747771
C 255	41	91.1	305	10	CG596498	CG596498	C 328	38	84.4	572	6	CF341423
C 256	41	91.1	378	1	AV655175	AV655175	C 329	38	84.4	575	6	CF248822
C 257	41	91.1	426	1	AL830731	AL830731	C 330	38	84.4	588	9	CF852793
C 258	41	91.1	517	11	DE122996	Oryzias_1	C 331	38	84.4	593	6	CF824888
C 259	41	91.1	556	3	BM036121	BM036121	C 332	38	84.4	595	6	CF248904
C 260	41	91.1	568	1	AL727624	AL727624	C 333	38	84.4	600	2	BE800090
C 261	41	91.1	581	3	BP199948	BP199948	C 334	38	84.4	614	6	CB375251

[illegible]

444	C 400	445	C 380	446	C 388	447	C 387	448	C 386	449	C 385	450	C 384	451	C 383	452	C 382	453	C 381	454	C 380	455	C 379	456	C 378	457	C 377	458	C 376	459	C 375	460	C 374	461	C 373	462	C 372	463	C 371	464	C 370	465	C 369	466	C 368	467	C 367	468	C 366	469	C 365	470	C 364	471	C 363	472	C 362	473	C 361	474	C 360	475	C 403	476	C 402	477	C 401	478	C 400	479	C 399	480	C 398	481	C 397	482	C 396	483	C 395	484	C 394	485	C 393	486	C 392	487	C 391	488	C 390	489	C 389	490	C 388	491	C 387	492	C 386	493	C 385	494	C 384	495	C 383	496	C 382	497	C 381	498	C 380	499	C 379	500	C 378	501	C 377	502	C 376	503	C 375	504	C 374	505	C 373	506	C 372	507	C 371	508	C 370	509	C 369	510	C 368	511	C 367	512	C 366	513	C 365	514	C 364	515	C 363	516	C 362	517	C 361	518	C 360	519	C 404	520	C 403	521	C 402	522	C 401	523	C 400	524	C 399	525	C 398	526	C 397	527	C 396	528	C 395	529	C 394	530	C 393	531	C 392	532	C 391	533	C 390	534	C 389	535	C 388	536	C 387	537	C 386	538	C 385	539	C 384	540	C 383	541	C 382	542	C 381	543	C 380	544	C 379	545	C 378	546	C 377	547	C 376	548	C 375	549	C 374	550	C 373	551	C 372	552	C 371	553	C 370	554	C 369	555	C 368	556	C 367	557	C 366	558	C 365	559	C 364	560	C 363	561	C 362	562	C 361	563	C 360	564	C 404	565	C 403	566	C 402	567	C 401	568	C 400	569	C 399	570	C 398	571	C 397	572	C 396	573	C 395	574	C 394	575	C 393	576	C 392	577	C 391	578	C 390	579	C 389	580	C 388	581	C 387	582	C 386	583	C 385	584	C 384	585	C 383	586	C 382	587	C 381	588	C 380	589	C 379	590	C 378	591	C 377	592	C 376	593	C 375	594	C 374	595	C 373	596	C 372	597	C 371	598	C 370	599	C 369	600	C 368	601	C 367	602	C 366	603	C 365	604	C 364	605	C 363	606	C 362	607	C 361	608	C 360	609	C 404	610	C 403	611	C 402	612	C 401	613	C 400	614	C 399	615	C 398	616	C 397	617	C 396	618	C 395	619	C 394	620	C 393	621	C 392	622	C 391	623	C 390	624	C 389	625	C 388	626	C 387	627	C 386	628	C 385	629	C 384	630	C 383	631	C 382	632	C 381	633	C 380	634	C 379	635	C 378	636	C 377	637	C 376	638	C 375	639	C 374	640	C 373	641	C 372	642	C 371	643	C 370	644	C 369	645	C 368	646	C 367	647	C 366	648	C 365	649	C 364	650	C 363	651	C 362	652	C 361	653	C 360	654	C 404	655	C 403	656	C 402	657	C 401	658	C 400	659	C 399	660	C 398	661	C 397	662	C 396	663	C 395	664	C 394	665	C 393	666	C 392	667	C 391	668	C 390	669	C 389	670	C 388	671	C 387	672	C 386	673	C 385	674	C 384	675	C 383	676	C 382	677	C 381	678	C 380	679	C 379	680	C 378	681	C 377	682	C 376	683	C 375	684	C 3
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C 519	36	80.0	351	5	BU431751	592	36	80.0	519	7	CN114991	CN114991
C 520	36	80.0	354	7	CO270062	593	36	80.0	519	9	A2433235	A2433235
C 521	36	80.0	356	8	CM603106	594	36	80.0	520	7	CR744847	CR744847
C 522	36	80.0	369	9	CN108604	595	36	80.0	521	7	CN101773	CN101773
C 523	36	80.0	369	9	AO243158	596	36	80.0	522	7	CN119290	EC0CA19D
C 524	36	80.0	370	7	CN106316	597	36	80.0	522	7	CN124542	EC0CA001
C 525	36	80.0	370	7	CN110426	598	36	80.0	523	7	CN101772	MS0256.B2
C 526	36	80.0	376	9	CC082877	599	36	80.0	523	7	CN101772	CN101772
C 527	36	80.0	381	3	BP735561	600	36	80.0	525	2	BE882216	BE882216
C 528	36	80.0	382	7	CN105590	601	36	80.0	527	2	BE458767	BU825740
C 529	36	80.0	383	7	CN088799	602	36	80.0	527	2	BE458767	EST14059
C 530	36	80.0	387	2	BM141271	603	36	80.0	527	7	CN120477	CN120477
C 531	36	80.0	390	2	BM412371	604	36	80.0	528	8	CN120477	UK12TG02
C 532	36	80.0	391	7	CO994884	605	36	80.0	528	1	A1545991	A1545991
C 533	36	80.0	398	6	CB707016	606	36	80.0	531	7	CN106089	CN106089
C 534	36	80.0	401	1	AA213791	607	36	80.0	532	8	CN104368	EC0CA25D
C 535	36	80.0	401	9	AO830829	608	36	80.0	532	8	DN487008	P081D05.3
C 536	36	80.0	401	9	AO904317	609	36	80.0	533	3	CN105095	CN105095
C 537	36	80.0	401	9	AZ050607	610	36	80.0	534	5	BU827139	BU827139
C 538	36	80.0	405	7	CN109181	611	36	80.0	536	7	CN114422	CN114422
C 539	36	80.0	406	6	CB807515	612	36	80.0	537	9	CE016806	CE016806
C 540	36	80.0	407	7	CN115490	613	36	80.0	538	1	AL927623	AL927623
C 541	36	80.0	408	3	BP925500	614	36	80.0	538	7	CN114292	EC0CA45D
C 542	36	80.0	409	7	CO270066	615	36	80.0	539	7	CN118309	CN118309
C 543	36	80.0	412	5	BO618684	616	36	80.0	540	9	CR928469	CR928469
C 544	36	80.0	412	6	CB801707	617	36	80.0	540	9	AO877860	HS_2152.B
C 545	36	80.0	414	5	BO617903	618	36	80.0	544	7	CN118110	CN118110
C 546	36	80.0	416	1	A1779915	619	36	80.0	545	7	AO877170	EC0CA28B
C 547	36	80.0	416	6	CB767746	620	36	80.0	549	1	AM621780	EST132578
C 548	36	80.0	423	1	A1190894	621	36	80.0	549	7	CN095858	CN095858
C 549	36	80.0	423	1	CN115491	622	36	80.0	550	3	BM529016	BM529016
C 550	36	80.0	425	1	A1497291	623	36	80.0	550	7	CN119801	CN119801
C 551	36	80.0	425	3	BI809535	624	36	80.0	550	7	CN119858	CN119858
C 552	36	80.0	426	9	AO444341	625	36	80.0	552	6	CA953478	SAV57D02.
C 553	36	80.0	429	3	BI433060	626	36	80.0	552	8	DT055486	AGENCOURT
C 554	36	80.0	431	2	BG135185	627	36	80.0	554	2	BE995683	EST14106
C 555	36	80.0	432	9	AO458488	628	36	80.0	557	7	CR432620	CR432620
C 556	36	80.0	433	6	CB759611	629	36	80.0	558	2	BE354465	EST355808
C 557	36	80.0	435	1	AW811331	630	36	80.0	558	8	BO597729	MI-P-A2-a
C 558	36	80.0	439	1	AL915855	631	36	80.0	558	5	CA388765	CA388765
C 559	36	80.0	446	8	DN492103	632	36	80.0	559	5	BT065466	BT065466
C 560	36	80.0	447	3	BI882955	633	36	80.0	559	7	CN108905	CN108905
C 561	36	80.0	447	7	CN074221	634	36	80.0	560	1	A1497360	A1497360
C 562	36	80.0	449	8	T96423	635	36	80.0	560	3	BU525099	BU525099
C 563	36	80.0	451	1	A1023586	636	36	80.0	560	7	CN082174	EC2BBA20C
C 564	36	80.0	453	8	DR875341	637	36	80.0	561	1	CN082301	CN082301
C 565	36	80.0	454	11	DE037146	638	36	80.0	564	7	AL965676	AL965676
C 566	36	80.0	460	6	CB737454	639	36	80.0	564	7	DN074222	EC0CBAA04
C 567	36	80.0	463	11	DE136921	640	36	80.0	564	7	DT093242	DT093242
C 568	36	80.0	465	9	CC841879	641	36	80.0	566	8	BE925854	BE925854
C 569	36	80.0	470	7	CN106425	642	36	80.0	566	8	DR896168	DR896168
C 570	36	80.0	471	8	DR875342	643	36	80.0	567	7	CN105157	CN105157
C 571	36	80.0	475	2	BE558057	644	36	80.0	567	7	CN105307	EC2CA27A
C 572	36	80.0	476	5	BO858578	645	36	80.0	568	3	BM529516	BM529516
C 573	36	80.0	477	3	BP903498	646	36	80.0	570	6	CB188859	CB188859
C 574	36	80.0	479	1	AJ457525	647	36	80.0	571	3	BU002196	BU002196
C 575	36	80.0	479	5	BU878410	648	36	80.0	571	3	BE915324	BE915324
C 576	36	80.0	483	3	CN114992	649	36	80.0	571	6	CD015852	CD015852
C 577	36	80.0	491	2	BF717871	650	36	80.0	572	6	BU529214	BU529214
C 578	36	80.0	491	2	BO597720	651	36	80.0	573	7	CN099377	CN099377
C 579	36	80.0	491	5	BU837167	652	36	80.0	575	7	CN082175	CN082175
C 580	36	80.0	492	8	DN490295	653	36	80.0	576	7	CR432621	CR432621
C 581	36	80.0	495	1	AM223900	654	36	80.0	577	8	CX780714	AGENCOURT
C 582	36	80.0	497	7	CN104369	655	36	80.0	577	8	CN106426	CN106426
C 583	36	80.0	500	5	BM116268	656	36	80.0	580	3	BM532980	BM532980
C 584	36	80.0	500	5	CN105306	657	36	80.0	580	7	CN076600	CN076600
C 585	36	80.0	503	5	BO510594	658	36	80.0	580	7	CN110427	CN110427
C 586	36	80.0	504	1	AA290567	659	36	80.0	581	6	CF102943	EC2CA35B
C 587	36	80.0	511	7	CO274429	660	36	80.0	581	6	CN093672	CN093672
C 588	36	80.0	512	6	CB400312	661	36	80.0	583	1	AM595479	AM595479
C 589	36	80.0	516	9	AO691311	662	36	80.0	584	7	CN099878	EC2CA16D
C 590	36	80.0	519	7	CN099376	663	36	80.0	585	1	AJ656696	AJ656696
C 591	36	80.0	519	7	CN105156	664	36	80.0	585	7	CN084599	EC2BBA24B

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665	36	80.0	586	8	CX694439	CX694439 ydc9a006.	c 738	36	80.0	663	5	BM318781	BM318781
C 666	36	80.0	587	1	AT1781459	AT1781459 EST262338	739	36	80.0	665	5	BM213645	BM213645
C 667	36	80.0	587	1	BM112051	BM112051 EST559587	740	36	80.0	665	5	BK262365	BK262365
C 668	36	80.0	588	9	CN087111	CN087117 EC2BBA28B	741	36	80.0	667	1	AT264817	AT264817
C 669	36	80.0	589	9	BH656435	BH656435 BOMWV377F	742	36	80.0	669	2	B2505098	B2505098
C 670	36	80.0	590	10	CE8442861	CE8442861 C19F-988-	743	36	80.0	671	10	AG127133	AG127133
C 671	36	80.0	590	10	CN091358	CN091358 EC2BBA34D	744	36	80.0	672	10	CN833757	CN833757
C 672	36	80.0	592	3	BP362058	BP362058 BP362058	745	36	80.0	674	5	B0603230	B0603230
C 673	36	80.0	594	7	CN106317	CN106317 EC2CA22B	746	36	80.0	675	5	B2440966	B2440966
C 674	36	80.0	595	1	AV957991	AV957991 AV957991	747	36	80.0	676	5	B2449563	B2449563
C 675	36	80.0	595	1	CN108605	CN108605 EC2CA32B	748	36	80.0	678	3	BU001063	BU001063
C 676	36	80.0	596	9	BZ206854	BZ206854 CH230-526	749	36	80.0	680	7	CX716164	CX716164
C 677	36	80.0	596	9	AL630355	AL630355 AL630355	750	36	80.0	684	5	BM213933	BM213933
C 678	36	80.0	597	5	BQ615424	BQ615424 fdb26c08.	751	36	80.0	685	9	BZ000604	BZ000604
C 679	36	80.0	598	6	CA779231	CA779231 MFL384.8	752	36	80.0	686	9	CC958715	CC958715
C 680	36	80.0	598	6	CB582935	CB582935 AMGNNUC:N	753	36	80.0	688	1	AW256822	AW256822
C 681	36	80.0	598	10	CZ188860	CZ188860 OA_BBA011	754	36	80.0	688	5	BK263921	BK263921
C 682	36	80.0	599	1	AM594942	AM594942 EK26f12.y	755	36	80.0	688	7	CO132929	CO132929
C 683	36	80.0	600	3	BI990895	BI990895 4082-64.M	756	36	80.0	690	8	CX643472	CX643472
C 684	36	80.0	600	6	CB582552	CB582552 AMGNNUC:N	757	36	80.0	690	8	DN899099	DN899099
C 685	36	80.0	600	7	CN118939	CN118939 EC2CA9BG	758	36	80.0	690	8	BZ006739	BZ006739
C 686	36	80.0	601	1	AL676115	AL676115 AL676115	759	36	80.0	692	5	BM689563	BM689563
C 687	36	80.0	602	9	BZ459560	BZ459560 BONPU687F	760	36	80.0	692	10	CL441074	CL441074
C 688	36	80.0	604	5	BX706547	BX706547 BX706547	761	36	80.0	694	8	BZ519703	BZ519703
C 689	36	80.0	604	5	BM2848721	BM2848721 EC2CA32D	762	36	80.0	696	8	DT059997	DT059997
C 690	36	80.0	604	9	BZ428721	BZ428721 BONEB60TR	763	36	80.0	696	9	BH755521	BH755521
C 691	36	80.0	605	2	BE942386	BE942386 EST421965	764	36	80.0	697	9	AZ098153	AZ098153
C 692	36	80.0	605	6	CB581627	CB581627 AMGNNUC:N	765	36	80.0	698	10	CMS46663	CMS46663
C 693	36	80.0	606	6	CB581271	CB581271 hbc39f12.	766	36	80.0	701	1	AM584642	AM584642
C 694	36	80.0	606	6	CF102947	CF102947 IPcGFr1.4	767	36	80.0	702	3	BM213466	BM213466
C 695	36	80.0	606	6	CV990651	CV990651 hbc39f12.	768	36	80.0	703	5	BH519418	BH519418
C 696	36	80.0	606	9	AO670292	AO670292 HS_5389.B	769	36	80.0	704	8	CX358689	CX358689
C 697	36	80.0	607	9	BH439596	BH439596 BOGOR32TR	770	36	80.0	704	8	DR403106	DR403106
C 698	36	80.0	608	8	CX780443	CX780443 AGENCOURT	771	36	80.0	704	9	BH793753	BH793753
C 699	36	80.0	608	10	CE327594	CE327594 C19F-988-	772	36	80.0	704	9	BH119975	BH119975
C 700	36	80.0	609	2	BI206117	BI206117 EST524157	773	36	80.0	706	8	DR398845	DR398845
C 701	36	80.0	609	3	BJ518923	BJ518923 BJ518923	774	36	80.0	711	9	BH460979	BH460979
C 702	36	80.0	610	5	BM284683	BM284683 BM284683	775	36	80.0	711	10	CE344241	CE344241
C 703	36	80.0	611	7	CN095859	CN095859 EC2CA10C	776	36	80.0	713	1	AM687479	AM687479
C 704	36	80.0	612	6	CB472985	CB472985 hmc3.B02.	777	36	80.0	713	9	BH511418	BH511418
C 705	36	80.0	613	7	CN095873	CN095873 EC2CA10C	778	36	80.0	714	9	BZ017165	BZ017165
C 706	36	80.0	613	7	CN109182	CN109182 EC2CA33B	779	36	80.0	715	2	BG127881	BG127881
C 707	36	80.0	615	10	CG158686	CG158686 PU1B078TB	780	36	80.0	719	9	CC087525	CC087525
C 708	36	80.0	617	7	CN076601	CN076601 EC2BBA12A	781	36	80.0	729	3	BM407961	BM407961
C 709	36	80.0	621	9	AZ964314	AZ964314 2M0233023	782	36	80.0	730	6	CB230219	CB230219
C 710	36	80.0	622	7	CN093673	CN093673 EC2BBA8CB	783	36	80.0	730	6	CK142645	CK142645
C 711	36	80.0	622	7	BJ523935	BJ523935 EC2BBA24B	784	36	80.0	730	11	DE106380	DE106380
C 712	36	80.0	625	3	CN084600	CN084600 EC2BBA24B	785	36	80.0	732	5	BU357601	BU357601
C 713	36	80.0	625	11	DE077612	DE077612 Oryzias.1	786	36	80.0	738	7	CK029504	CK029504
C 714	36	80.0	626	6	CB578073	CB578073 AMGNNUC:N	787	36	80.0	740	8	DN172096	DN172096
C 715	36	80.0	627	8	DN649064	DN649064 G6709.69	788	36	80.0	744	7	CKR69681	CKR69681
C 716	36	80.0	629	7	CN082302	CN082302 EC2BBA20D	789	36	80.0	745	8	DN833827	DN833827
C 717	36	80.0	630	7	CN102763	CN102763 EC2CA32B	790	36	80.0	752	5	BU345436	BU345436
C 718	36	80.0	630	7	CN108096	CN108096 EC2CA31B	791	36	80.0	752	9	BH534733	BH534733
C 719	36	80.0	633	7	CN100544	CN100544 EC2CA17D	792	36	80.0	752	10	AG484711	AG484711
C 720	36	80.0	634	3	BJ520612	BJ520612 EC2CA33B	793	36	80.0	754	7	CK025268	CK025268
C 721	36	80.0	635	7	CN112895	CN112895 EC2CA39B	795	36	80.0	756	10	CMS46932	CMS46932
C 722	36	80.0	636	7	CX362343	CX362343 JGI_XZT42	796	36	80.0	756	7	CV239322	CV239322
C 723	36	80.0	637	8	BM341041	BM341041 BM341041	797	36	80.0	757	10	AG591785	AG591785
C 724	36	80.0	641	5	DE084868	DE084868 Oryzias.1	798	36	80.0	759	9	BH452545	BH452545
C 725	36	80.0	644	11	AM128739	AM128739 f636h01.y	799	36	80.0	763	8	DN632536	DN632536
C 726	36	80.0	649	2	BB653036	BB653036 BO1BM18TF	800	36	80.0	764	7	CU379586	CU379586
C 727	36	80.0	650	9	CC943865	CC943865 ND1.131H1	801	36	80.0	765	10	AG536094	AG536094
C 728	36	80.0	651	2	AL899320	AL899320 AL899320	802	36	80.0	766	7	CO927591	CO927591
C 729	36	80.0	652	1	CR753214	CR753214 DKFZ469I	803	36	80.0	766	7	CC970326	CC970326
C 730	36	80.0	655	1	BM406368	BM406368 EST580791	804	36	80.0	767	9	BZ520070	BZ520070
C 731	36	80.0	655	1	BM406368	BM406368 MT-P-E3.a	805	36	80.0	769	9	DN769703	DN769703
C 732	36	80.0	659	3	BM406368	BM406368 GR_BA43E	807	36	80.0	770	8	DN835674	DN835674
C 733	36	80.0	660	7	BM214540	BM214540 BM214540	808	36	80.0	771	8	DN771972	DN771972
C 734	36	80.0	663	5	BM214540	BM214540	809	36	80.0	772	3	BH691494	BH691494
C 735	36	80.0					810	36	80.0				
C 736	36	80.0						36	80.0				
C 737	36	80.0						36	80.0				

C 811	36	80.0	774	4	CN60G9XT	CR708901 Tetradon	C 884	36	80.0	892	9	CC003651	CC003651 PUD6637D
C 812	36	80.0	774	9	B2061928	B2061928 1Jq72905	C 885	36	80.0	895	10	CG958396	CG958396 MB63U02TR
C 813	36	80.0	775	8	DN834001	DN834001 AGENCOURT	C 886	36	80.0	896	2	B6179307	B6179307 60231027
C 814	36	80.0	776	8	DN766133	DN766133 AGENCOURT	C 887	36	80.0	896	7	CO915165	CO915165 AGENCOURT
C 815	36	80.0	778	3	BH557483	BH557483 BOGJUT58TR	C 888	36	80.0	897	7	CN832588	CN832588 AGENCOURT
C 816	36	80.0	780	3	BI908127	BI908127 603067423	C 889	36	80.0	917	10	CG205672	CG205672 PUFUF74TD
C 817	36	80.0	780	7	CV486862	CV486862 AGENCOURT	C 890	36	80.0	918	10	C2939052	C2939052 259193 To
C 818	36	80.0	782	8	DN765964	DN765964 AGENCOURT	C 891	36	80.0	924	7	CK176696	CK176696 EST766016
C 819	36	80.0	782	8	DN767167	DN767167 AGENCOURT	C 892	36	80.0	924	8	DN836260	DN836260 AGENCOURT
C 820	36	80.0	783	8	DN764812	DN764812 AGENCOURT	C 893	36	80.0	930	6	CF265987	CF265987 AGENCOURT
C 821	36	80.0	783	8	DN833932	DN833932 AGENCOURT	C 894	36	80.0	932	7	CK865572	CK865572 AGENCOURT
C 822	36	80.0	784	1	AM004353	AM004353 AM004353	C 895	36	80.0	934	7	CK285610	CK285610 EST748332
C 823	36	80.0	785	2	BG588660	BG588660 EST490469	C 896	36	80.0	934	7	CK870860	CK870860 AGENCOURT
C 824	36	80.0	785	8	DN956036	DN956036 AGENCOURT	C 897	36	80.0	940	7	CK866313	CK866313 AGENCOURT
C 825	36	80.0	787	8	DN768395	DN768395 AGENCOURT	C 898	36	80.0	941	7	CK869539	CK869539 AGENCOURT
C 826	36	80.0	788	8	DN768957	DN768957 AGENCOURT	C 899	36	80.0	942	7	CN024895	CN024895 AGENCOURT
C 827	36	80.0	788	8	DN770073	DN770073 AGENCOURT	C 900	36	80.0	942	9	CC123294	CC123294 ND1.81F18
C 828	36	80.0	789	8	DN771600	DN771600 AGENCOURT	C 901	36	80.0	944	5	BU162006	BU162006 AGENCOURT
C 829	36	80.0	790	8	DN770937	DN770937 AGENCOURT	C 902	36	80.0	947	7	CK865531	CK865531 AGENCOURT
C 830	36	80.0	791	8	DN860832	DN860832 Tab15a08	C 903	36	80.0	949	10	CG929232	CG929232 EDCBV70TR
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C 832	36	80.0	793	2	BG581983	BG581983 EST483720	C 905	36	80.0	982	11	CNS05561	AL351442 Tetradon
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C 834	36	80.0	797	8	DN765186	DN765186 AGENCOURT	C 907	36	80.0	1028	10	CNS0272R	AL184140 Tetradon
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C 836	36	80.0	801	8	DN770486	DN770486 AGENCOURT	C 909	36	80.0	1050	11	CNS079YX	AL435519 T7 end of
C 837	36	80.0	803	8	DN766957	DN766957 AGENCOURT	C 910	36	80.0	1052	10	CG698922	CG698922 ZMBBC011
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C 839	36	80.0	811	9	BH681250	BH681250 BOHTE20TR	C 912	36	80.0	1101	7	CK025645	CK025645 AGENCOURT
C 840	36	80.0	813	9	CK872250	CK872250 AGENCOURT	C 913	36	80.0	1118	10	CG935532	CK025532 EDCU40TR
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C 845	36	80.0	820	7	CK289667	CK289667 EST752389	C 918	36	80.0	1508	8	DN722763	AK044557 Mus muscu
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C 847	36	80.0	824	9	CK714119	CK714119 ZF201-P00	C 920	36	80.0	3146	4	AK035902	AK035902 Mus muscu
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C 849	36	80.0	828	9	CK142634	CK142634 AGENCOURT	C 922	35	77.8	209	7	CK758698	CK758698 pam01-11m
C 850	36	80.0	829	6	CAS82815	CAS82815 EST002490	C 923	35	77.8	213	3	BJ518712	BJ518712 BJS18712
C 851	36	80.0	832	1	AM944027	AM944027 LP03982.3	C 924	35	77.8	217	1	AA447954	AA447954 xz11f08.x
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C 855	36	80.0	835	6	CA475101	CA475101 AGENCOURT	C 928	35	77.8	261	7	CO597815	CO597815 DG8-15312
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C 861	36	80.0	851	7	CN832906	CN832906 AGENCOURT	C 934	35	77.8	285	1	AV074251	AV074251 AV074251
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C 863	36	80.0	852	7	CK710088	CK710088 ZF201-P00	C 936	35	77.8	293	7	CO596794	CO596794 DG8-13561
C 864	36	80.0	855	8	CK440126	CK440126 JGI XZG59	C 937	35	77.8	302	10	AY413662	AY413662 Pan. t10g1
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C 866	36	80.0	859	7	CN319967	CN319967 AGENCOURT	C 939	35	77.8	305	2	BR174571	BR174571 MYB3406A
C 867	36	80.0	859	9	BZ791322	BZ791322 PUFAR17TB	C 940	35	77.8	309	1	BB138183	BB138183 BBI38183
C 868	36	80.0	859	9	CC398589	CC398589 PUDU84TD	C 941	35	77.8	311	1	AF090128	AF090128 AF090128
C 869	36	80.0	862	6	CA975491	CA975491 AGENCOURT	C 942	35	77.8	311	3	BM060318	BM060318 KSO101340
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C 875	36	80.0	868	6	CD460974	CD460974 F909_0301	C 948	35	77.8	339	9	AQ081824	AQ081824 RPCI11-55
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965 35 77.8 385 5 BQ608625
966 35 77.8 387 5 BQ608625
967 35 77.8 390 7 BQ608625
968 35 77.8 392 1 AM87231
969 35 77.8 394 1 AM87231
970 35 77.8 396 1 BQ00867
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ALIGNMENTS

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DEFINITION PM1-MT0143-100701-007-e12 MT0143 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ336306
VERSION BQ336306.1 GI:2092407
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W.J., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsushima, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.J.G.
Laboratory of Cancer Genetics

```

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FEATURES
source
1. 149
/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN
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Pred. No.: 5.86 Length: 149
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DB 91 CCAGATGATATTTCTACGAGAGTT 117

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DEFINITION MR4-ET0140-220101-004-h09_1 ET0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ331200
VERSION BQ331200.1 GI:20972241
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W.J., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsushima, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922

```


Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM04&c2=NR4-ET0140-220101-004-h09.1&c3=2001-01-22&c4=1)
Seq primer: puc 18 forward.

FEATURES
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Location/Qualifiers

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Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Score: 6.17 Length: 156
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US-10-757-745-2_COPY_145_153 (1-9) x BQ331200 (1-156)

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DEFINITION PM0-IT0018-091100-001-d12 IT0018 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF768814
VERSION BF768814.1 GI:12116818
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 247)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM04&c2=PM0-IT0018-
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High quality sequence start: 9
High quality sequence stop: 246.
Location/Qualifiers

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/note="Organ: epid tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Score: 10.4 Length: 247
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Best Local Similarity: 100.0% Conservative: 0
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Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF768814 (1-247)

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DB 110 CCAGATGTCATATTTCTACAGAGATT 136

RESULT 4
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DEFINITION EST28102 Cerebellum II Homo sapiens CDNA 5' end, mRNA sequence.
ACCESSION AA325145
VERSION AA325145.1 GI:1977400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 252)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weissstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wei, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, V.L., Geoghegan, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merriek, J.M.,
Moreno-Palander, R.E., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterbeck, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinhe, D., Feng, D.-F., Ferrite, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Praser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@igr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

Bouice

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ORIGIN

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DB:	1
Gaps:	0
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US-10-757-745-2_COPY_145_153 (1-9) x AA325145 (1-252

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RESULT 5	BF992136	LOCUS	DEFINITION
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	OV7-GN0201-301000-454-b08 GN0201	Homo sapiens	CDNA, mRNA sequence.

REFERENCE
AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT:

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Tel: +55-11-2704822
Fax: +55-11-2707801
Email: asimperson@ludwig.org.br
This sequence was derived from the FAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/genetics/gethtml2.pl?tbl=QV3&ec2=QV3-GN0201>
(http://www.ludwig.org.br/genetics/gethtml2.pl?tbl=QV3-GN0201)
Seq primer: puc 18 forward
High quality sequence stop: 296.

FEATURES
SOURCE

```

/dev_stage="Adult"
/clone_lib="GN201"
/host="O3gan"
/vector="pUC18"
/site_1="
  Note: This is a mini-library was made by cloning
  small pieces derived from ORSRTS PCR (U.S. Letters Patent
  application No. 196,716 - Ludwig Institute for Cancer
  Research) profiles into the pUC 18 vector. Reverse
  transcription of tissue mRNA and cDNA amplification were
  performed under low stringency conditions."

```

ORIGIN

Alignment Scores:

pred. No.:	12.8	Length:	296
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatch:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF992136 (1-296,

Qy 1 ProAspValIlePheLeuGlnGluVal 9
Db 99 CCAGATGTGATATTTCTACAGGAGTT 1.25

LOCUS	BP92133	313 bp	mRNA	linear	EST 23-JAN-2001
DEFINITION	OV3-GN0201-301000-454-g09	GN0201	Homo sapiens	cDNA, mRNA sequence.	

REFERENCE AUTHORS

TITLE
JOURNAL
PUBMED
COMMENT

Simpson, A. Cloning of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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Tel: +55-11-2707001
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.hcrg.org.br/scripts/gschtml2.pl?tl=GV3ctc2-QV3-GN0201
30100045:908ct3:2008-10-30&ct=1)
30100045:908ct3:2008-10-30 forward
High quality sequence start: 45
High quality sequence stop: 311.
Location/Qualifiers
1..313
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0201"
/note="Organ: placenta normal; Vector: puc19; Site: 1;
smat; Site: 2; smat; A mini-library was made by cloning
primers derived from ORESTES PCR (U.S. Letters Patent

Application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	13.6	45.00	9	0	0	0
Percent Similarity:	100.0%	100.0%	0	0	0	0
Best Local Similarity:	100.0%	100.0%	0	0	0	0
Query Match:	2	2	0	0	0	0

US-10-757-745-2_COPY_145_153 (1-9) x BE694706 (1-313)

Qy 1 ProaPva111epheleuGIngluV1 9
 Db 99 CCAGATGATATTTCTACAGAGATT 125

RESULT 7

LOCUS BE694706 368 bp mRNA linear EST 11-SHP-2000
 DEFINITION PMO-BT0757-140800-006-d10 BT0757 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE694706
 VERSION BE694706.1 GI:10081866
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo

REFERENCE

1 (bases 1 to 368)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Coelta, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

PUBMED

COMMENT

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 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESB/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=kt2=PMO-BT0757-140800-006-d10&ct=2000-08-14&f4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 37
 High quality sequence stop: 368.
 Location/Qualifiers

FEATURES

source

1..368
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_id="BT0757"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	16.4	45.00	9	0	0	0
Percent Similarity:	100.0%	100.0%	0	0	0	0
Best Local Similarity:	100.0%	100.0%	0	0	0	0
Query Match:	2	2	0	0	0	0

US-10-757-745-2_COPY_145_153 (1-9) x BE694706 (1-368)

Qy 1 ProaPva111epheleuGIngluV1 9
 Db 176 CCAGATGATATTTCTACAGAGATT 150

RESULT 8

LOCUS AV659558 368 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV659558 GLC Homo sapiens cDNA clone GLCFYD04 3', mRNA sequence.
 ACCESSION AV659558
 VERSION AV659558.1 GI:9880572
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo

REFERENCE

1 (bases 1 to 368)
 Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, O., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL

PUBMED

COMMENT

CONTACT: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 Location/Qualifiers

FEATURES

source

1..368
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_id="GLCFYD04"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SQR"
 /clone_id="GLC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	17.4	45.00	9	0	0	0
Percent Similarity:	100.0%	100.0%	0	0	0	0
Best Local Similarity:	100.0%	100.0%	0	0	0	0
Query Match:	1	1	0	0	0	0

US-10-757-745-2_COPY_145_153 (1-9) x AV659558 (1-368)

Qy 1 ProaPva111epheleuGIngluV1 9
 Db 315 CCAGATGATATTTCTACAGAGATT 341

ORIGIN

RESULT 9
LOCUS AV661333 394 bp mRNA linear EST 16-JAN-2002
DEFINITION AV661333 GLC Homo sapiens CDNA clone GICGRD01_3', mRNA sequence.
ACCESSION AV661333
VERSION AV661333.1 GI:9882347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 394)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Ou,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z., and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
11752456
JOURNAL
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201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
location/Qualifiers
1..394
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GICGRD01"
/issue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1fb="GLC"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 17.7 Length: 394
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x AV661333 (1-394)
QY 1 Proaapvalllpheleuglnluval 9
DB 221 CCGATGTGATATTCTACAGAGTT 247
RESULT 10
LOCUS BQ332322 413 bp mRNA linear EST 17-MAY-2002
DEFINITION MR4-ET0140-240501-015-d11 ET0140 Homo sapiens CDNA, mRNA sequence.
ACCESSION BQ332322
VERSION BQ332322.1 GI:20973745
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 413)
Dias,Neto,E., Garcia Corra,R., Verjovskij-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Metukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V., and
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
JOURNAL
PUBMED
COMMENT Contact: Simpson A.J.G.
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/HICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4ct2=MR4-ET0140-
240501-015-d11ct3=2001-05-24ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 6
FEATURES
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location/Qualifiers
1..413
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1fb="ET0140"
/note="Organ: lung; tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cdna amplification were performed under
low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 18.7 Length: 413
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BQ332322 (1-413)
QY 1 Proaapvalllpheleuglnluval 9
DB 53 CCGATGTGATATTCTACAGAGTT 79
RESULT 11
LOCUS BF853399 419 bp mRNA linear EST 16-JAN-2001
DEFINITION MR3-EN0087-191200-015-807 EN0087 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF853399
VERSION BF853399.1 GI:12241143
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 419)
Dias Neto,E., Garcia Corraes,R., Verjovskij-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL
PUBMED
COMMENT

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&ct2=MR3-CN0147-
1912001-015-a07&ct3=2000-12-19&ct4=1)
Seg primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 419.
Location/Qualifiers
1..419
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1b="EN0087"
/note="Organ: lung_normal; Vector: puc18; Site_1: Smal;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 19 Length: 419
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF653399 (1-419)

Qy 1 Proaepval11ephleugIngluval 9
|||||
Db 59 CCAGATGATATTTCTACAGAGATT 85

RESULT 12
LOCUS BG982044 422 bp mRNA linear EST 12-JUN-2001
DEFINITION MR3-CN0147-120201-011-h12 CN0147 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG982044
VERSION BG982044.1 GI:14384779
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 422)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bale, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
PUBMED
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&ct2=MR3-CN0147-
120201-011-h12&ct3=2001-02-12&ct4=1)
Seg primer: puc 18 forward
High quality sequence start: 47
High quality sequence stop: 422.
Location/Qualifiers
1..422
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1b="CN0147"
/note="Organ: colon_normal; Vector: puc18; Site_1: Smal;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 19.2 Length: 422
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG982044 (1-422)

Qy 1 Proaepval11ephleugIngluval 9
|||||
Db 342 CCAGATGATATTTCTACAGAGATT 316

RESULT 13
LOCUS BQ582059 429 bp mRNA linear EST 20-JUN-2002
DEFINITION 1112c11.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6029589
5' similar to TR:095551 095551 D030M3.3 ;, mRNA sequence.
ACCESSION BQ582059
VERSION BQ582059.1 GI:21494955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 429)

REFERENCE

AUTHORS

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemshka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V.,
Williams, T., Jackson, Y. and Bowers, Y.

TITLE

Unpublished (2000)
Other ESTs: 1112c11.x1

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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557

Email: dmelton@biochem.harvard.edu
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 Bluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
 University Genome Sequencing Center for information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)
 Seq primer: -40RP from G1bco.
 Location/Qualifiers
 1..429
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6029589"
 /issue_type="Insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Human Insulinoma"
 /note="Organ: Pancreas; Vector: pBluescript SK-; Site_1:
 XhoI; Site_2: EcoRI; Constructed with lambda Zapri system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 please contact Hiroshi Inoue, MD/PhD for further
 information on this library (Metabolism Division, Permut
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:
 Pred. No.: 19.5 Length: 429
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BQ582059 (1-429)

QY 1 Proaapvalilepheelengingluval 9
 DB 376 CCAGATGATGATTTCTACAGAAATT 402

RESULT 14
 BQ32331/c 435 bp mRNA linear EST 17-MAY-2002
 LOCUS MR4-ET0140-240501-015-g10 ET0140 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BQ32331
 ACCESSION BQ32331.1 GI:20973758
 VERSION EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 435)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Coats,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
 JOURNAL PUBMED
 COMMENT
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
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 Brazil
 Tel: +55-11-2704822
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4-ET0140-
 240501-015-g10c3=2001-05-24c4a1)
 Seq primer: puc 18 forward
 High quality sequence start: 132
 High quality sequence stop: 435.
 Location/Qualifiers
 1..435
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ET0140"
 /note="Organ: Lung tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORSTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 19.8 Length: 435
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BQ32331 (1-435)

QY 1 Proaapvalilepheelengingluval 9
 DB 355 CCAGATGATGATTTCTACAGAAATT 329

RESULT 15
 BF768820/c 437 bp mRNA linear EST 12-JAN-2001
 LOCUS PM0-IT0018-091100-001-a01 IT0018 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF768820
 ACCESSION BF768820.1 GI:12116824
 VERSION EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 437)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Coats,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
 JOURNAL PUBMED
 COMMENT
 CONTACT: Simpson A.J.G.
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 Ludwig Institute for Cancer Research
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 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM0-IT0018-
 091100-001-a01c3=2000-11-09c4a1)
 Seq primer: puc 18 forward

High quality sequence start: 28
High quality sequence stop: 437.
Location/Qualifiers

FEATURES

source

1. 437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="T0018"
/note="Organ: epid.tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	19.9	Length:	437
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF768820 (1-437)

Qy 1 ProaPVal1lePheLeuGlnGluVal 9

DB 357 CCAGATGATATTTCTACAGGAACTT 331

RESULT 16

US-10-757-745-2_COPY_145_153 (1-9) x BF768820 (1-437)

LOCUS BG982029 440 bp mRNA linear EST 12-JUN-2001

DEFINITION MR3-CN0147-120201-011-b10 CN0147 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG982029

VERSION BG982029.1 GI:14384764

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 440)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT 10737800

CONTACT: Simpson A.J.G.

LABORATORY: Laboratory of Cancer Genetics

INSTITUTE: Ludwig Institute for Cancer Research

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TEL: +55-11-2704922

FAX: +55-11-2707001

EMAIL: asimpson@ludwig.org.br

PROJECT: This entry was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL: (http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&e2=MR3-CN0147-120201-011-b10&t3=2001-02-12&t4=1)

SEG PRIMER: puc 18 forward

HIGH QUALITY SEQUENCE STOP: 440.

/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"
/note="Organ: colon, normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	20.1	Length:	440
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG982029 (1-440)

Qy 1 ProaPVal1lePheLeuGlnGluVal 9

DB 360 CCAGATGATATTTCTACAGGAACTT 334

RESULT 17

US-10-757-745-2_COPY_145_153 (1-9) x BG982029 (1-440)

LOCUS BG982036 440 bp mRNA linear EST 12-JUN-2001

DEFINITION MR3-CN0147-120201-011-d12 CN0147 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG982036

VERSION BG982036.1 GI:14384771

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 440)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT 10737800

CONTACT: Simpson A.J.G.

LABORATORY: Laboratory of Cancer Genetics

INSTITUTE: Ludwig Institute for Cancer Research

ADDRESS: Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

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FAX: +55-11-2707001

EMAIL: asimpson@ludwig.org.br

PROJECT: This entry was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL: (http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&e2=MR3-CN0147-120201-011-d12&t3=2001-02-12&t4=1)

SEG PRIMER: puc 18 forward

HIGH QUALITY SEQUENCE STOP: 440.

FEATURES

source

1. 440
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"
/note="Organ: colon, normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	20.1	Length:	440
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG982036 (1-440)

QY

1 ProaSpValliepheleugIngluval 9
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360 CCAGATGATATTCTTACGAGAGTT 334

RESULT 18

BF992415 441 bp mRNA linear EST 18-JAN-2001
LOCUS PM1-MT0143-041100-002-f12 MT0143 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF992415
ACCESSION BF992415.1 GI:12283874
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

AUTHORS
1 (bases 1 to 441)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

JOURNAL
PUBMED
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&c=PM1-MT0143-
041100-002-f12&c3=2000-11-13&c4=1)
Seq primer: puc 18 forward
High quality sequence stop: 441.
Location/Qualifiers

FEATURES

source

1..441
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0143"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	20.1	Length:	441
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF992415 (1-441)

QY

1 ProaSpValliepheleugIngluval 9
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81 CCAGATGATATTCTTACGAGAGTT 107

RESULT 19

BF993925 441 bp mRNA linear EST 18-JAN-2001
LOCUS PM1-MT0143-131100-004-g08 MT0143 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF993925
ACCESSION BF993925.1 GI:12285384
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

AUTHORS
1 (bases 1 to 441)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

JOURNAL
PUBMED
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&c=PM1-MT0143-
131100-004-g08&c3=2000-11-13&c4=1)
Seq primer: puc 18 forward
High quality sequence stop: 441.
Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0143"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 20.1 Length: 441
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893925 (1-441)

QY 1 ProaPVal11lePheLeuGInG1Val 9
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 DB 81 CCAGATGATATTTCTACAGAACTT 107

RESULT 20
 BF893187 444 bp mRNA linear EST 18-JAN-2001
 LOCUS PM1-MT0143-101100-003-h07 MT0143 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF893187
 ACCESSION BF893187.1 GI:12284646
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 444)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
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 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
 JOURNAL
 PUBMED
 COMMENT 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
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 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-MT0143-
 101100-003-h07&c3=2000-11-10&c4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 444.
 Location/Qualifiers
 1..444
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1ib="MT0143"
 /note="Organ: marrow; Vector: puc18; Site 1: Sma1; Site 2:
 Sma1; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 20.3 Length: 444
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893187 (1-444)

QY 1 ProaPVal11lePheLeuGInG1Val 9
 |||||
 |||||

DB 84 CCAGATGATATTTCTACAGAACTT 110

RESULT 21
 BF891509 447 bp mRNA linear EST 18-JAN-2001
 LOCUS PM1-MT0143-281000-001-h02 MT0143 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF891509
 ACCESSION BF891509.1 GI:12282981
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 447)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
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TITLE
 JOURNAL
 PUBMED
 COMMENT 10737800
 Contact: Simpson A.J.G.
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 Ludwig Institute for Cancer Research
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 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-MT0143-
 281000-001-h02&c3=2000-10-28&c4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 27
 High quality sequence stop: 447.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1ib="MT0143"
 /note="Organ: marrow; Vector: puc18; Site 1: Sma1; Site 2:
 Sma1; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 20.5 Length: 447
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF891509 (1-447)

QY 1 ProaPVal11lePheLeuGInG1Val 9
 |||||
 DB 88 CCAGATGATATTTCTACAGAACTT 114

RESULT 22
 BF773259/c 453 bp mRNA linear EST 12-JAN-2001
 LOCUS

DEFINITION PM0-IT0018-151200-002-d10 IT0018 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF773259
VERSION BF773259.1 GI:12121159
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 453)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brijones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Proc.Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT
JOURNAL Contact: Simpson A.J.G.
PUBMED Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM0&t2=PM0-IT0018-151200-002-d10&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence stop: 133.
Location/Qualifiers
source
1..453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/def_stage="Adult"
/clone_id="IT0018"
/note="Organ: epid.tumor; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORFESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
Alignment Scores:
Pred. No.: 20.8 Length: 453
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 2
US-10-757-745-2_COPY_145_153 (1-9) x BF773259 (1-453)
ORIGIN
1 Proaapvialllepheuglmglyva 9
Db 373 CCAGATGTGATATTTCTACAGGAAGTT 347
RESULT 23
LOCUS BQ315535/c 453 bp mRNA linear EST 16-MAY-2002
DEFINITION PM0-IT0018-151200-002-d06 IT0018 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ315535
VERSION BQ315535.1 GI:20874720
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 453)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brijones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT
JOURNAL Contact: Simpson A.J.G.
PUBMED Laboratory of Cancer Genetics
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM0&t2=PM0-IT0018-151200-002-d06&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 20.
Location/Qualifiers
source
1..453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="IT0018"
/note="Organ: epid.tumor; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORFESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
Alignment Scores:
Pred. No.: 20.8 Length: 453
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3
US-10-757-745-2_COPY_145_153 (1-9) x BQ315535 (1-453)
ORIGIN
1 Proaapvialllepheuglmglyva 9
Db 373 CCAGATGTGATATTTCTACAGGAAGTT 347
RESULT 24
LOCUS BQ982031/c 454 bp mRNA linear EST 12-JUN-2001
DEFINITION MR3-CN0147-120201-011-b12 CN0147 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ982031
VERSION BQ982031.1 GI:14384766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 454)

AUTHORS
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
 10737800

COMMENT
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 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-CN0147-120201-011-b1&t3=2001-02-12&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 15
 High quality sequence stop: 453.
 Location/Qualifiers

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 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CN0147"
 /note="Organ: colon_normal; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 20.8 Length: 454
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG982031 (1-454)

QY
 1 Proaepvalillepheleugingluval 9

DB
 373 CCAGATGTGATATTTCTACAGAGGTT 347

RESULT 25
 BF996980 456 bp mRNA linear EST 23-JAN-2001
 LOCUS BF996980
 DEFINITION QV3-GN0201-081100-468-c10 GN0201 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF996980
 VERSION BF996980.1 GI:12403303
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 456)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

REFERENCE
 AUTHORS

TITLE
 Simpson, A.J.

JOURNAL
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

PUBMED
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

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 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV3&t2=QV3-GN0201-081100-468-c10&t3=2000-11-08&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 456.
 Location/Qualifiers

FEATURES
 source
 1..456
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="GN0201"
 /note="Organ: placenta_normal; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 20.9 Length: 456
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF996980 (1-456)

QY
 1 Proaepvalillepheleugingluval 9

DB
 376 CCAGATGTGATATTTCTACAGAGTT 350

RESULT 26
 BQ332321 456 bp mRNA linear EST 17-MAY-2002
 LOCUS BQ332321
 DEFINITION MR4-ET0140-240501-015-d10 ET0140 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BQ332321
 VERSION BQ332321.1 GI:20973744
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 456)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

REFERENCE
 AUTHORS

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
 10737800

COMMENT
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&ct2=MR4-ET0140-
240501-015-d10&ct3=2001-05-24&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 456.
Location/Qualifiers
1..456
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0140"
/note="Organ: lung tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	20.9	Length:	456
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BQ32321 (1-456)

QY 1 Proaspvalillepheleungingluval 9
DB 96 CCAGATGATATTTCTACAGAGATT 122

RESULT 27

LOCUS BQ36782 458 bp mRNA linear EST 21-MAY-2002
DEFINITION BQ36782
ACCESSION BQ36782
VERSION BQ36782.1 GI:21042296
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 459)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matuskuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

REFERENCE
AUTHORS

TITLE
JOURNAL
PUBMED
COMMENT

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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV3&ct2=QV3-ON0201-
081100-437-c05&ct3=2000-11-08&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 12.
Location/Qualifiers
1..458
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ON0201"
/note="Organ: placenta normal; Vector: puc18; Site 1:
Sma1; Site 2: Sma1; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	21	Length:	458
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BQ36782 (1-458)

QY 1 Proaspvalillepheleungingluval 9
DB 378 CCAGATGATATTTCTACAGAGATT 352

RESULT 28

LOCUS BQ982034 459 bp mRNA linear EST 12-JUN-2001
DEFINITION BQ982034
ACCESSION BQ982034
VERSION BQ982034.1 GI:14384769
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 459)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matuskuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

REFERENCE
AUTHORS

TITLE
JOURNAL
PUBMED
COMMENT

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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&ct2=MR3-ON0147-
120201-011-c09&ct3=2001-02-12&ct4=1)
Seq primer: puc 18 forward

High quality sequence start: 19
High quality sequence stop: 459
Location/Qualifiers

FEATURES

1..459
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"
/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	21.1	Length:	459
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG982034 (1-459)

OY 1 ProapVal11lePhelengIngluVal 9
DB 379 CCAGATGATATTTCTACAGAGATT 353

RESULT 29

BF93150 460 bp mRNA linear EST 18-JUN-2001
LOCUS PM1-MT0143-101100-003-b07 MT0143 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF93150
ACCESSION BF93150.1 GI:12284609
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

1 (bases 1 to 460)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
PUBMED
COMMENT
10737800
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-MT0143-
101100-003-b07&c3=2000-11-10&c4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 434.
Location/Qualifiers

FEATURES

1..460
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0143"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Pred. No.:	21.1	Length:	460
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF93150 (1-460)

OY 1 ProapVal11lePhelengIngluVal 9
DB 100 CCAGATGATATTTCTACAGAGATT 126

RESULT 30

BG982012 461 bp mRNA linear EST 12-JUN-2001
LOCUS MR3-CN0147-120201-011-b03 CN0147 Homo sapiens cDNA, mRNA sequence.
DEFINITION BG982012
ACCESSION BG982012.1 GI:14384747
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

1 (bases 1 to 461)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
PUBMED
COMMENT
10737800
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&c2=MR3-CN0147-
120201-011-b03&c3=2001-02-12&c4=1)
Seq primer: puc 18 forward
High quality sequence stop: 191.
Location/Qualifiers

FEATURES

source

1..461
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"
/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products

derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	21.2	Length:	463
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG982012 (1-461)

QY 1 ProaepValIlePheLeuGInGluVal 9
|||||
DB 381 CCAGATGTGATATTCTCGACGAGGTT 355

RESULT 31

BF852284 463 bp mRNA linear EST 16-JAN-2001
LOCUS MR3-EN0087-121200-007-d01 EN0087 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF852284
ACCESSION BF852284
VERSION BF852284.1 GI:12239655
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 463)
Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Brites M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-EN0087-121200-007-d01&t3=2000-12-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 463.
Location/Qualifiers

FEATURES

source 1..463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0087"
/note="Organ: lung normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 21.3
Score: 45.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 2
Length: 463
Matches: 9
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF852284 (1-463)

QY 1 ProaepValIlePheLeuGInGluVal 9
|||||
DB 95 CCAGATGTGATATTCTACGAGAGTT 121

RESULT 32

BF852788 463 bp mRNA linear EST 16-JAN-2001
LOCUS MR3-EN0087-151200-012-a09 EN0087 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF852788
ACCESSION BF852788
VERSION BF852788.1 GI:12240532
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 463)
Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Brites M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-EN0087-151200-012-a09&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 31
High quality sequence stop: 463.
Location/Qualifiers

FEATURES

source 1..463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0087"
/note="Organ: lung normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 21.3
Score: 45.00
Percent Similarity: 100.0%
Length: 463
Matches: 9
Conservative: 0

Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 2
Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF852788 (1-463)

QY 1 Proapval111epheleunglingluyal 9
DB 363 CCAGATGATATTTCTACAGAAAGTT 357

RESULT 33
LOCUS BF893919 463 bp mRNA linear EST 18-JAN-2001
DEFINITION PM1-MT0143-131100-004-e06 MT0143 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF893919
VERSION BF893919.1 GI:12285378
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 463)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, M. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

TITLE
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPER/P/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-MT0143-
131100-004-e06&c3=2000-11-13&c4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 463.
Location/Qualifiers
1..463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_11b="MT0143"
/note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 21.3
Score: 45.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 2
Length: 463
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893919 (1-463)

QY 1 Proapval111epheleunglingluyal 9
DB 103 CCAGATGATATTTCTACAGAAAGTT 129

RESULT 34
LOCUS BF893924 471 bp mRNA linear EST 18-JAN-2001
DEFINITION PM1-MT0143-131100-004-g07 MT0143 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF893924
VERSION BF893924.1 GI:12285383
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 471)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, M. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

TITLE
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPER/P/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-MT0143-
131100-004-g07&c3=2000-11-13&c4=1)
Seq primer: puc 18 forward
High quality sequence start: 33
High quality sequence stop: 471.
Location/Qualifiers
1..471
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_11b="MT0143"
/note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

FEATURES

source

1..471
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_11b="MT0143"
/note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 21.7
Score: 45.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 2
Length: 471
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893924 (1-471)

QY 1 Proapval111epheleunglingluyal 9
DB 391 CCAGATGATATTTCTACAGAAAGTT 365

RESULT 35
CR543841 471 bp mRNA linear EST 07-JUL-2004
LOCUS DKEZP45900742.r1.459 (synonym: pcor1) Pongo pygmaeus CDNA clone
DEFINITION DKEZP45900742.5, mRNA sequence.
ACCESSION CR543841
VERSION CR543841.1 GI:49895253
KEYWORDS EST
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pongo

REFERENCE
AUTHORS Bloembergen, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B., Amid, C.,
Oestge, A., Robe, G., Yan, M. and Wiemann, S.
TITLE Pongo pygmaeus RNA (Bloembergen, H., Boecker, M., Brandt, P., et al.)
JOURNAL Unpublished (2004)
COMMENT MIPB

FEATURES
source
1..471
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone=DKEZP45900742"
/cdate=DKEZP45900742"
/issue_type="core"
/seq_start=1
/seq_end=471
/seq_start=1
/seq_end=471
/note="Vector: pspori1_Sfi1; Site_1: Sfi1A; Site_2: Sfi1B"

ORIGIN
Alignment Scores:
Pred. No.: 21.7 Length: 471
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR543841 (1-471)

QY 1 PROSPVALLIAPHLEUNGICLVA1 9
DB 434 CCAGATGCAATATTTCTACGAGAGTT 460

RESULT 36
CR120234 473 bp mRNA linear EST 20-JUN-2003
LOCUS K-EST0167337 LBSCKO Homo sapiens CDNA clone LBSCKO-29-F06 5', mRNA
DEFINITION K-EST0167337 LBSCKO Homo sapiens CDNA clone LBSCKO-29-F06 5', mRNA
ACCESSION CR120234
VERSION CR120234.1 GI:27946036
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo

REFERENCE
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim, YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@kribb.re.kr
Plate: 29 row: F column: 06
High quality sequence stop: 473.

FEATURES
source
1..473
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LBSCKO-29-F06"
/cdate="M"
/seq_start="1"
/seq_end="473"
/seq_start="1"
/seq_end="473"
/note="Vector: pT7T3-PAC; Site_1: EcoRI;
Site_2: NotI. The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996) Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN
Alignment Scores:
Pred. No.: 21.8 Length: 473
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR120234 (1-473)

QY 1 PROSPVALLIAPHLEUNGICLVA1 9
DB 382 CCAGATGCAATATTTCTACGAGAGTT 408

RESULT 37
AT150554 480 bp mRNA linear EST 20-JUN-2002
LOCUS ch04a01.y1 Normal Human Trabecular Bone Cells Homo sapiens CDNA
DEFINITION ch04a01.y1 Normal Human Trabecular Bone Cells Homo sapiens CDNA
ACCESSION AT150554
VERSION AT150554.1 GI:5128818
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo

REFERENCE
AUTHORS Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G., Yang, L.M.,
Becker, R., Sternberg, S.M., Green, E.D., Powell, J.L., Yang, L.M.,
Rodey, P.G., Hochkiss, R.N. and Francmann, C.A.
TITLE The Skeletal Genome Anatomy Project
JOURNAL Unpublished (1997)
COMMENT Contact: Libin Jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 3000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).

Plate: 04 row: a column: 01
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1..480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NH7BC_cn04a01"
/sex="Female"
/tissue_type="Bone"
/cell_type="Tribecular Bone Cells"
/lab_host="SURE"
/clone_id="Normal Human Tribecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI;
Library constructed by Dr. Marian Young and Dr. Pamela
Gehron Robey (NIDCR)"

ORIGIN
Alignment Scores:
Pred. No.: 22.2 Length: 480
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AT750554 (1-480)

Qy 1 ProaPVal11lePheLeuGInGluVal 9
Db 427 CCAGATGATATTCTTACAGAACTT 453

RESULT 38
LOCUS AA486032 485 bp mRNA linear EST 06-MAR-1998
DEFINITION ab40b10.r1 StrataGene Hela cell 83 937216 Homo sapiens cDNA clone
IMAGE:843259 5', mRNA sequence.
ACCESSION AA486032
VERSION AA486032.1 GI:2216248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 485)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Stepcoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-MC1 human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.jnl.gov) for further information.
Insert length: 1913 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence Bcop: 444.
Location/Qualifiers
1..485
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:843259"
/sex="Female"
/dev_stage="Hela S3 cell line"
/lab_host="SOUR (kanamycin resistant)"
/clone_id="Stratagene Hela cell 83 937216"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. Hela S3
epithelioid carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; uni-ZAP XR
Vector -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."

ORIGIN
Alignment Scores:
Pred. No.: 22.4 Length: 485
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AA486032 (1-485)

Qy 1 ProaPVal11lePheLeuGInGluVal 9
Db 423 CCAGATGATATTCTTACAGAACTT 449

RESULT 39
LOCUS AJ681912 491 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ681912 CSEORAN04 Sus scrofa cDNA clone C0001797_I20, mRNA
sequence.
ACCESSION AJ681912
VERSION AJ681912.1 GI:49414502
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 491)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS+). R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..491
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001797_I20"
/tissue_type="uterus"
/clone_id="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

ORIGIN
Alignment Scores:
Pred. No.: 22.8 Length: 491
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AJ681912 (1-491)

QY 1 Proaapva111epheleung1n1uval 9
DB 127 CCAGATGTGATTTCTACAGAAATT 153

RESULT 40
BI016235/c 491 bp mRNA linear EST 13-JUN-2001
DEFINITION MR4-ET0140-130301-009-a09 ET0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI016235
VERSION BI016235.1 GI:14420306
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 491)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.P., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

JOURNAL
COMMENT Contact: Simpson, A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&cl2=MR4-ET0140-
130301-009-a09&cl3=2001-03-13&cl4=1)
130301-009-a09&cl3=2001-03-13&cl4=1)
Hed primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 232.
Location/Qualifiers
1 491
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0140"
/note="Organ: Lung tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESSES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Alignment Scores: 22.8 Length: 491
Pred. No.: 45.00 Matches: 9
Score: 100.0% Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BI016235 (1-491)

QY 1 Proaapva111epheleung1n1uval 9
DB 410 CCAGATGTGATTTCTACAGAAATT 384

RESULT 41
BM846221 530 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0125204 S13KMS5 Homo sapiens cDNA clone S13KMS5-59-C04 5',
DEFINITION mRNA sequence.
ACCESSION BM846221
VERSION BM846221.1 GI:19202620
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 530)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.U., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseungemall.kribb.re.kr
Plate: 59 row: C column: 04
High quality sequence start: 530.
High quality sequence stop: 530.
Location/Qualifiers
1 530
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-59-C04"
/tissue="myeloma"
/cell_line="RMS-5"
/lab_host="TOP10F"
/clone_lib="S13KMS5"
/note="Vector: PCNS; Site 1: BcoRI; Site 2: NotI. The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then deccapped linker I site by
pyrophosphatase (TAP). The deccapped linker I site by
ligated with DNA-RNA linker including BcoRI site by
treatment of T4 RNA ligase and the linker strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was digested to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of BcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
TOP10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

ORIGIN
Alignment Scores: 24.8 Length: 530
Pred. No.: 45.00 Matches: 9
Score: 100.0% Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BM846221 (1-530)

QY 1 Proaapva111epheleung1n1uval 9
DB 437 CCAGATGTGATTTCTACAGAAATT 463

RESULT 42
LOCUS CN298921 534 bp mRNA linear EST 16-MAY-2004

```

DEFINITION 17000531590248 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN2889921
VERSION CN2889921.1 GI:47315335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1. (bases 1 to 534)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Flisk, G.J.,
            Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
            Lebkowski, J. and Stanton, L.W.
            Transcriptional characterization elucidates signaling networks that
            control human ES cell growth and differentiation
            Nat. Biotechnol. 22 (6), 707-716 (2004)
TITLE Transcriptional characterization elucidates signaling networks that
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
            Regenerative Medicine
            Genon Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@genon.com
FEATURES
            source
            1. 534
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /issue_type="embryonic stem cells, embryoid bodies
            derived from H1, H7 and H9 cells"
            /clone_lib="GRN_EB"
            /note="oligo dt primed, full-length enriched cDNA library
            from embryoid body outgrowth derived from h9 cell lines
            H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
            conditions."
ORIGIN
Alignment Scores:
Pred. No.: 25 Length: 534
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x CN2889921 (1-534)
QY 1 ProAapVallilepheLengIngluVal 9
Db |||||
40 CCAGATGATGATATTCTACAGAAATT 66
RESULT 43
BG541031 546 bp mRNA linear EST 03-APR-2001
LOCUS 602570190F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694374 5',
DEFINITION mRNA sequence.
ACCESSION BG541031
VERSION BG541031.1 GI:13533264
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1. (bases 1 to 546)
AUTHORS NIH-MGC http://imgc.ncl.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.

```

```

cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://imgc.ncl.nih.gov
Plate: L10M1518 row: d column: 23
High quality sequence spot: 545.
FEATURES
            source
            1. 546
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone_lib="IMAGE:4694374"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NIH MGC 77"
            /note="Organ: Lung; Vector: pMDR-LTR (Clontech); Site 1:
            Sfil (ggcgccctcgcc); Site 2: Sfil (ggccattatggc); 5' and
            3' adaptors were used in cloning as follows: 5' adaptor
            sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
            5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.9
            kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH-MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 25.7 Length: 546
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BG541031 (1-546)
QY 1 ProAapVallilepheLengIngluVal 9
Db |||||
39 CCAGATGATGATATTCTACAGAAATT 65
RESULT 44
AM669835 549 bp mRNA linear EST 25-APR-2001
LOCUS 113421 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION AM669835
ACCESSION AM669835
VERSION AM669835.1 GI:7526349
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1. (bases 1 to 549)
AUTHORS Smith, R.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
            Casab, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
            Bennett, G.L., Heaton, M.P., Jaeger, W.W., Rohrer, G.A.,
            Chitko-McKown, C.G., Pettea, G., Holt, I., Karaycheva, S., Liang, F.,
            Quackenbush, J. and Keele, J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
JOURNAL libraries and construction of a gene index for cattle
PUBMED 11282978
COMMENT Contact: Smith TPJ
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smithr@mail.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.

```

PCR Primers
 FORWARD: AGGAACAGCATGACCAT
 BACKWARD: GTTTCACGACGACG
 Plate: 108 row: M column: 18
 Seq primer: ATTGACGACGACATG.
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 1 549
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 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="MDH10B"
 /clone_1lb="MARC 1BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 library made from pooled tissue from lymph node, ovary,
 fat, hypothalamus, and pituitary."

ORIGIN
 Alignment Scores:
 Pred. No.: 25 9 Length: 549
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0
 DB: 1
 US-10-757-745-2_COPY_145_153 (1-9) x AW669835 (1-549)
 Oy 1 ProApyA111epheLeuGInG1uV1 9
 Db 498 CCGATGTGATATTCTACAGGAAGTC 524

RESULT 45
 BP220985 554 bp mRNA linear EST 15-SEP-2004
 LOCUS BP220985 Sugano cDNA library, colon Homo sapiens cDNA clone
 DEFINITION COL06450, mRNA sequence.
 ACCESSION BP220985.1 GI:52093890
 VERSION BP220985.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo
 1 (bases 1 to 554)
 Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)
 JOURNAL
 PUBMED
 15342556
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers
 1..554
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="COL06450"
 /tissue_type="colon"
 /clone_1lb="Sugano cDNA library, colon"

ORIGIN
 Alignment Scores:
 Pred. No.: 26 1 Length: 554
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0

DB: 3 Gaps: 0
 US-10-757-745-2_COPY_145_153 (1-9) x BP220985 (1-554)
 Oy 1 ProApyA111epheLeuGInG1uV1 9
 Db 342 CCGATGTGATATTCTACAGGAAGTC 368

RESULT 46
 BP226620 565 bp mRNA linear EST 15-SEP-2004
 LOCUS BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
 DEFINITION clone DMC03190, mRNA sequence.
 ACCESSION BP226620.1 GI:52099525
 VERSION BP226620.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo
 1 (bases 1 to 565)
 Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)
 JOURNAL
 PUBMED
 15342556
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers
 1..565
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DMC03190"
 /clone_1lb="Sugano cDNA library, dermoid cancer"
 /note="dermoid cancer"

ORIGIN
 Alignment Scores:
 Pred. No.: 26 7 Length: 565
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP226620 (1-565)
 Oy 1 ProApyA111epheLeuGInG1uV1 9
 Db 434 CCGATGTGATATTCTACAGGAAGTC 460

RESULT 47
 BP220508 566 bp mRNA linear EST 15-SEP-2004
 LOCUS BP220508 Sugano cDNA library, colon Homo sapiens cDNA clone
 DEFINITION COL03160, mRNA sequence.
 ACCESSION BP220508.1 GI:52093413
 VERSION BP220508.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo
 1 (bases 1 to 566)
 Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL03160"
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ORIGIN

Alignment Scores:

Pred. No.:	26.8	Length:	566
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BP220508 (1-566)

Qy 1 Proaepval11epheuglgnlval 9
|||||
DB 352 CCAGATGATATTTCTACAGAGATT 378

RESULT 48
BP257211 568 bp mRNA linear EST 16-SBP-2004
LOCUS BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone
DEFINITION HRT00430, mRNA sequence.
ACCESSION BP257211 GI:52172441
VERSION BP257211.1 GI:52172441
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 568)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
source
1..568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRT00430"
/tissue_type="heart"
/clone_lib="Sugano cDNA library, heart"

ORIGIN

Alignment Scores:

Pred. No.:	26.9	Length:	568
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP257211 (1-568)

Qy 1 Proaepval11epheuglgnlval 9
|||||
DB 403 CCAGATGATATTTCTACAGAGATT 429

RESULT 49
BM172060 570 bp mRNA linear EST 04-DEC-2001
LOCUS imagec3.2001/sml233bdf41.x1 NIH_MGC_76 Homo sapiens cDNA clone
DEFINITION IMAGE:4700059 5', mRNA sequence.
ACCESSION BM172060
VERSION BM172060.1 GI:17311623
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 570)
Kale, P. I., Harsch, T. J., Folta, P. A., Nelson, D. O., Sanders, C. G. and Prange, C. K.
The I.M.A.G.E. Consortium quality control effort: clone resequencing for verification
Unpublished (2001)
Other ESTs: BG533717
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the correct orientation), as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having 100 or more base pairs with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For information on obtaining this clone, please contact info@image.llnl.gov.
Plate: LBCM1533 row: a column: 20
Seq primer: -21m13
High quality sequence stop: 570.
Location/Qualifiers

FEATURES
source
1..570
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4700059"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 76"
/note="Organ: Liver; Vector: pDNR-LIB (Clontech); Site: 1: 5'fll (ggcgccgcgcgc); Site 2: 5'fll (ggcctatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	27	Length:	570
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BM172060 (1-570)

QY 1 ProaPVAL11epheleunglunyal 9

DB 285 CCAAGATGATATTTCTACAGAAAGTT 311

RESULT 50

LOCUS BP221518

DEFINITION BP221518 Sugano cDNA library, colon Homo sapiens cDNA clone

ACCESSION BP221518

VERSION BP221518.1 GI:52094423

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,S., Nakai,K. and Sugano,S

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT

CONTACT: Yutaka Suzuki

DEPARTMENT OF VIROLOGY

INSTITUTE OF MEDICAL SCIENCE, UNIVERSITY OF TOKYO

4-6-1, SHIROKANE, MINATOKU, TOKYO 108-8639, JAPAN

EMAIL: yusuzuki@ims.u-tokyo.ac.jp

FEATURES

source

1..570

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="COL09203"

/issue_type="colon"

/clone_lib="Sugano cDNA library, colon"

ORIGIN

Alignment Scores:

Pred. No.: 27

Score: 45.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 3

Length: 570

Matches: 9

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP221518 (1-570)

QY 1 ProaPVAL11epheleunglunyal 9

DB 341 CCAAGATGATATTTCTACAGAAAGTT 367

RESULT 51

LOCUS BP258309

DEFINITION BP258309 Sugano cDNA library, heart Homo sapiens cDNA clone

ACCESSION BP258309

VERSION BP258309.1 GI:52173539

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,S., Nakai,K. and Sugano,S

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT

CONTACT: Yutaka Suzuki

DEPARTMENT OF VIROLOGY

INSTITUTE OF MEDICAL SCIENCE, UNIVERSITY OF TOKYO

4-6-1, SHIROKANE, MINATOKU, TOKYO 108-8639, JAPAN

EMAIL: yusuzuki@ims.u-tokyo.ac.jp

FEATURES

source

1..570

/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="HRT03149"

/issue_type="heart"

/clone_lib="Sugano cDNA library, heart"

ORIGIN

Alignment Scores:

Pred. No.: 27

Score: 45.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 3

Length: 572

Matches: 9

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP258309 (1-570)

QY 1 ProaPVAL11epheleunglunyal 9

DB 78 CCAAGATGATATTTCTACAGAAAGTT 104

RESULT 52

LOCUS BP62485

DEFINITION BP62485 Sugano cDNA library, small intestine Homo sapiens cDNA clone HS107111, mRNA sequence.

ACCESSION BP62485

VERSION BP62485.1 GI:52177716

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,S., Nakai,K. and Sugano,S

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT

CONTACT: Yutaka Suzuki

DEPARTMENT OF VIROLOGY

INSTITUTE OF MEDICAL SCIENCE, UNIVERSITY OF TOKYO

4-6-1, SHIROKANE, MINATOKU, TOKYO 108-8639, JAPAN

EMAIL: yusuzuki@ims.u-tokyo.ac.jp

FEATURES

source

1..572

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/clone="HS107111"

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Best Local Similarity: 100.0%

Query Match: 3

Length: 572

Matches: 9

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP262485 (1-572)

QY 1 Proaapvaliilepheleuglncgluval 9
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Db 389 CCAGATGATATTTCTACAGAGATT 415

RESULT 53

LOCUS AU279894 573 bp mRNA linear EST 31-JUL-2003
DEFINITION AU279894 CHONS2 Homo sapiens cDNA clone CHONS2002038 5', mRNA
sequence.
ACCESSION AU279894
VERSION AU279894.1 GI:28299121
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE

1 (bases 1 to 573)
Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R.,
Isogai, T., Hata, J., Tomoya, Y. and Umezawa, A.
Redefinition of differentiated chondrocytes and
chondrogenesis of human bone marrow stromal cells via chondrosphere
formation with expression profiling by large-scale cDNA analysis
Exp. Cell Res. 288 (1), 35-50 (2003)

JOURNAL

PUBMED
12878157
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1537-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3875
Fax: 81-438-52-3986
Email: genomics@hri.co.jp

COMMENT

HRI human cDNA Project, Sugiyama, T.; Makamatsu, A.; Irie, R.;
Umezawa, A.; Fukuma, M.; Kusakari, S.; Hata, J.; Ishii, S.; Yamamoto, J.;
Isono, Y.; Saito, K.; Nakamura, Y.; Masuhio, Y.; Nagai, K.; Isogai, T.
HRI human cDNA project, cDNA library construction & 5'-end one
pass sequencing: Helix Research Institute.
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/note="Vector: pME18SFL3"

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Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AU279894 (1-573)

QY 1 Proaapvaliilepheleuglncgluval 9
|||||
Db 470 CCAGATGATATTTCTACAGAGATT 496

RESULT 54

LOCUS BP221260 573 bp mRNA linear EST 15-SEP-2004
DEFINITION BP221260 Sugano cDNA library, colon Homo sapiens cDNA clone
COL08083, mRNA sequence.
ACCESSION BP221260
VERSION BP221260.1 GI:52094165
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE 1 (bases 1 to 573)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL

PUBMED
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
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Email: yusuzuki@ims.u-tokyo.ac.jp.

COMMENT

Location/Qualifiers
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Score: 45.00 Matches: 9
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Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP221260 (1-573)

QY 1 Proaapvaliilepheleuglncgluval 9
|||||
Db 355 CCAGATGATATTTCTACAGAGATT 381

RESULT 55

LOCUS BP261500 573 bp mRNA linear EST 16-SEP-2004
DEFINITION BP261500 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS103816, mRNA sequence.
ACCESSION BP261500
VERSION BP261500.1 GI:52176731
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE 1 (bases 1 to 573)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL

PUBMED
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

COMMENT

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/clone_lib="Sugano CDNA library, small intestine"
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FEATURES

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/db_xref="taxon:9606"
/clone="HS105008"
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Alignment Scores:

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Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BP261787 (1-580)

OY 1 ProaPVal11epheugIngluVal 9

DB 368 CCAGATGTGATTTCTACAGGAAGTT 394

RESULT 59

BP274368

LOCUS BP274368 Sugano cDNA library, kidney Homo sapiens cDNA clone
DEFINITION KDN00894, mRNA sequence.
ACCESSION BP274368
VERSION BP274368.1 GI:52188100
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 580)
Suzuki,Y., Yamashita,R., Hirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 27.5
Score: 45.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 1
Length: 581
Matches: 9
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

JOURNAL

PUBMED

15342556
Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

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Alignment Scores:

Pred. No.:	27.5	Length:	580
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BP274368 (1-580)

OY 1 ProaPVal11epheugIngluVal 9

DB 453 CCAGATGTGATTTCTACAGGAAGTT 479

RESULT 60

AV717253

LOCUS AV717253 DCB Homo sapiens cDNA clone DCBMA04 5', mRNA sequence.
DEFINITION AV717253
ACCESSION AV717253
VERSION AV717253.1 GI:10814405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 581)
Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 27.6
Score: 45.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 1
Length: 581
Matches: 9
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AV717253 (1-581)

OY 1 ProaPVal11epheugIngluVal 9

DB 276 CCAGATGTGATTTCTACAGGAAGTT 302

RESULT 61

BP207751

LOCUS BP207751 Sugano cDNA library, coronary artery smooth muscle cell
DEFINITION BP207751
ACCESSION BP207751
VERSION BP207751.1 GI:52064157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Hirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL

PUBMED

REFERENCE

AUTHORS

15342556
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Institute of Medical Science, University of Tokyo
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Email: ysuzuki@ims.u-tokyo.ac.jp.

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 34

PUBMED 15342556
Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/mol_type="mRNA"
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ORIGIN

Alignment Scores:
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP207751 (1-581)

QY 1 ProkaryoticPhenylalanyl 9
DB 341 CCAGATGTGATTTCTACAGAGATT 367

RESULT 62
BP225088 581 bp mRNA linear EST 15-SEP-2004
LOCUS BP225088 Sugano CDNA library, lymphocyte Daudi Homo sapiens CDNA
DEFINITION BP225088 DAI05184, mRNA sequence.
BP225088
VERSION BP225088.1 GI:52097993
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo

REFERENCE 1 (bases 1 to 581)

Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
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Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
Source Location/Qualifiers

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/clone="DAI05184"
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/clone_lib="Sugano CDNA library, lymphocyte Daudi"
/note="Burkitt's lymphoma"

ORIGIN

Alignment Scores:
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Score: 45.00 Matches: 9
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP225088 (1-581)

QY 1 ProkaryoticPhenylalanyl 9
DB 454 CCAGATGTGATTTCTACAGAGATT 480

RESULT 63
BP262101 581 bp mRNA linear EST 16-SEP-2004
LOCUS BP262101 Sugano CDNA library, small intestine Homo sapiens CDNA
DEFINITION BP262101 HS105893, mRNA sequence.
BP262101
ACCESSION BP262101.1 GI:52177332
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo

REFERENCE 1 (bases 1 to 581)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
Source Location/Qualifiers

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ORIGIN

Alignment Scores:
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Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP262101 (1-581)

QY 1 ProkaryoticPhenylalanyl 9
DB 61 CCAGATGTGATTTCTACAGAGATT 87

RESULT 64
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LOCUS BP262638 Sugano CDNA library, small intestine Homo sapiens CDNA
DEFINITION BP262638 HS105756, mRNA sequence.
BP262638
ACCESSION BP262638.1 GI:52177869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo

REFERENCE 1 (bases 1 to 581)

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mitsushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp.
Location/Qualifiers

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ORIGIN

Alignment Scores:
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Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP262638 (1-581)

QY 1 ProabpVal11lephLeugInglVal 9
DB 350 CCAGATGATGATTTCTACAGAGATT 376

RESULT 65
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LOCUS BP270744 Sugano cDNA library, small intestine Homo sapiens CDNA
DEFINITION clone KAR05146, mRNA sequence.
ACCESSION BP270744
VERSION BP270744.1 GI:52220093
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 581)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mitsushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp.
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN

Alignment Scores:
Pred. No.: 27.6 Length: 581
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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US-10-757-745-2_COPY_145_153 (1-9) x BP349936 (1-581)

QY 1 ProabpVal11lephLeugInglVal 9
DB 210 CCAGATGATGATTTCTACAGAGATT 236

RESULT 67
BP379659 581 bp mRNA linear EST 21-SEP-2004
LOCUS BP379659 Sugano cDNA library, uterus Homo sapiens CDNA clone
DEFINITION WMD06642, mRNA sequence.
ACCESSION BP379659
VERSION BP379659.1 GI:52412762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP270744 (1-581)

QY 1 ProabpVal11lephLeugInglVal 9
DB 341 CCAGATGATGATTTCTACAGAGATT 367

RESULT 66
BP349936 581 bp mRNA linear EST 17-SEP-2004
LOCUS BP349936 Sugano cDNA library, brain Homo sapiens CDNA clone
DEFINITION SZR06923, mRNA sequence.
ACCESSION BP349936
VERSION BP349936.1 GI:52279921
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 581)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mitsushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
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1..581
/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN

Alignment Scores:
Pred. No.: 27.6 Length: 581
Score: 45.00 Matches: 9
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Query Match: 100.0% Indels: 0
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US-10-757-745-2_COPY_145_153 (1-9) x BP349936 (1-581)

QY 1 ProabpVal11lephLeugInglVal 9
DB 210 CCAGATGATGATTTCTACAGAGATT 236

RESULT 67
BP379659 581 bp mRNA linear EST 21-SEP-2004
LOCUS BP379659 Sugano cDNA library, uterus Homo sapiens CDNA clone
DEFINITION WMD06642, mRNA sequence.
ACCESSION BP379659
VERSION BP379659.1 GI:52412762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.

ORIGIN

pooled and then subtracted with porcine ST fibroblast RNA to create a subtracted porcine Peyer's patch library of approximately 6,000 clones with an average insert size of 1.0 kbp."

Alignment Scores:

Pred. No.:	27.6	Length:	581
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CB286391 (1-581)

Qy 1 ProaspVall1lePheLeuGIngluVal 9

Db 265 CCAGATGTGATATTTCTACAGGAGTT 291

RESULT 69

BM507091 582 bp mRNA linear EST 15-FEB-2002

LOCUS ih24h01.y1 Human insulinoma Homo sapiens cDNA 5' similar to

DEFINITION TR:095551 095551 DJ30M3.3; mRNA sequence.

ACCESSION

BM507091

VERSION

BM507091.1 GI:18678234

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 582)

AUTHORS

Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, R., Lemishka, I., Scease, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blaisstein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Carstens, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T., Jackson, Y., and Bowers, Y.

TITLE

Endocrine Pancreas Consortium

JOURNAL

Unpublished (2000)

COMMENT

Other ESTs: ih24h01.x1

FEATURES

source

ORIGIN

1.582

FEATURES

source

ORIGIN

1.582

FEATURES

source

ORIGIN

1.582

FEATURES

source

ORIGIN

1.582

FEATURES

source

ORIGIN

Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110. Note: this is a Washington University Pancreas EST project library."

Alignment Scores:

Pred. No.:	27.6	Length:	582
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BM507091 (1-582)

Qy 1 ProaspVall1lePheLeuGIngluVal 9

Db 235 CCAGATGTGATATTTCTACAGGAGTT 261

RESULT 70

BP219740 582 bp mRNA linear EST 15-SEP-2004

LOCUS BP219740 Sugano cDNA library, caudate nucleus Homo sapiens cDNA

DEFINITION clone CNR08985, mRNA sequence.

ACCESSION

BP219740.1 GI:52092643

VERSION

BP219740.1 GI:52092643

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 582)

AUTHORS

Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, R., Lemishka, I., Scease, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blaisstein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Carstens, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T., Jackson, Y., and Bowers, Y.

TITLE

Endocrine Pancreas Consortium

JOURNAL

Unpublished (2000)

COMMENT

Other ESTs: ih24h01.x1

FEATURES

source

ORIGIN

1.582

FEATURES

source

ORIGIN

1.582

FEATURES

source

ORIGIN

1.582

FEATURES

source

ORIGIN

1.582

FEATURES

source

ORIGIN

1.582

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ACCESSION BP233592 GI:52106502
VERSION BP233592.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
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/clone="HCR00774"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_id="Sugano cDNA library, coronary artery
endothelial cell"
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Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conserved: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3
US-10-757-745-2_COPY_145_153 (1-9) x BP233592 (1-582)
QY 1 Proapvalli11epheleunglinglva1 9
Db 448 CCAGATGATGATTTCTACAGAGAGTT 474
RESULT 72
LOCUS BP234218 582 bp mRNA linear EST 15-SEP-2004
DEFINITION BP234218 Sugano cDNA library, coronary artery endothelial cell Homo
sapiens cDNA clone HCR02378, mRNA sequence.
ACCESSION BP234218
VERSION BP234218.1 GI:52107128
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
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/db_xref="taxon:9606"
/clone="HCR02378"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_id="Sugano cDNA library, coronary artery
endothelial cell"
ORIGIN
Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conserved: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3
US-10-757-745-2_COPY_145_153 (1-9) x BP234218 (1-582)
QY 1 Proapvalli11epheleunglinglva1 9
Db 460 CCAGATGATGATTTCTACAGAGAGTT 486
RESULT 73
LOCUS BP261141 582 bp mRNA linear EST 16-SEP-2004
DEFINITION BP261141 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS102806, mRNA sequence.
ACCESSION BP261141
VERSION BP261141.1 GI:52176372
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS102806"
/tissue_type="small intestine"
/clone_id="Sugano cDNA library, small intestine"
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Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conserved: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3
US-10-757-745-2_COPY_145_153 (1-9) x BP261141 (1-582)
QY 1 Proapvalli11epheleunglinglva1 9
Db 339 CCAGATGATGATTTCTACAGAGAGTT 365
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RESULT 74
BP261789
LOCUS BP261789 582 bp mRNA linear EST 16-SEP-2004
DEFINITION BP261789 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS105013, mRNA sequence.
ACCESSION BP261789
VERSION BP261789.1 GI:52177020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS105013"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN
Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP261789 (1-582)

QY 1 ProaSpVal11lePhelengInguVal 9
|||||
Db 61 CCAGATGATATTTCTACAGAACTT 87

RESULT 75
BP263516
LOCUS BP263516 582 bp mRNA linear EST 16-SEP-2004
DEFINITION BP263516 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS111929, mRNA sequence.
ACCESSION BP263516
VERSION BP263516.1 GI:52178747
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAR02166"
/tissue_type="small intestine"
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FEATURES
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1..582
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/db_xref="taxon:9606"
/clone="HS111929"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

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Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP270415 (1-582)

QY 1 ProaSpVal11lePhelengInguVal 9
|||||
Db 431 CCAGATGATATTTCTACAGAACTT 457

RESULT 76
BP270415
LOCUS BP270415 582 bp mRNA linear EST 17-SEP-2004
DEFINITION BP270415 Sugano cDNA library, small intestine Homo sapiens cDNA
clone KAR02166, mRNA sequence.
ACCESSION BP270415
VERSION BP270415.1 GI:52219764
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..582
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/db_xref="taxon:9606"
/clone="KAR02166"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

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RESULT 77
BP275810          582 bp mRNA linear EST 16-SEP-2004
LOCUS             BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone
DEFINITION        BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone
ACCESSION         BP275810
VERSION           BP275810.1 GI:52189542
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Homiidae; Homo.
REFERENCE          Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS           Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE             Sequence comparison of human and mouse genes reveals a homologous
                  block structure in the promoter regions
JOURNAL           Genome Res. 14 (9), 1711-1718 (2004)
PUBMED            15342556
COMMENT           Contact: Yutaka Suzuki
                  Department of Virology
                  Institute of Medical Science, University of Tokyo
                  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                  Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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                  /mol_type="mRNA"
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                  /clone_lib="Sugano cDNA library, kidney"

ORIGIN
Alignment Scores:
Pred. No.:        27.6      Length:      582
Score:            45.00     Matches:      9
Percent Similarity: 100.0%   Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:      100.0%     Indels:      0
DB:               3         Gaps:         0

US-10-757-745-2_COPY_145_153 (1-9) x BP275810 (1-582)
OY               1 Prokaryotic|lepheng|n|u|v|a| 9
Db               422 CCAGATGATGATATTTCTACAGGAAAGTT 448

RESULT 78
BP195721          583 bp mRNA linear EST 14-SEP-2004
LOCUS             BP195721 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION        BP195721 Sugano cDNA library, brain Homo sapiens cDNA clone
ACCESSION         BP195721
VERSION           BP195721.1 GI:52039998
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Homiidae; Homo.
REFERENCE          Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS           Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE             Sequence comparison of human and mouse genes reveals a homologous
                  block structure in the promoter regions
JOURNAL           Genome Res. 14 (9), 1711-1718 (2004)
PUBMED            15342556
COMMENT           Contact: Yutaka Suzuki
                  Department of Virology
                  Institute of Medical Science, University of Tokyo
                  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                  Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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                  /clone="HS105902"
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                  /clone_lib="Sugano cDNA library, small intestine"

ORIGIN
Alignment Scores:
Pred. No.:        27.7      Length:      583
Score:            45.00     Matches:      9
Percent Similarity: 100.0%   Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:      100.0%     Indels:      0
DB:               3         Gaps:         0

US-10-757-745-2_COPY_145_153 (1-9) x BP262103 (1-583)
OY               1 Prokaryotic|lepheng|n|u|v|a| 9
Db               490 CCAGATGATGATATTTCTACAGGAAAGTT 516

RESULT 79
BP262103          583 bp mRNA linear EST 16-SEP-2004
LOCUS             BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION        BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
ACCESSION         BP262103
VERSION           BP262103.1 GI:52177334
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Homiidae; Homo.
REFERENCE          Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS           Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE             Sequence comparison of human and mouse genes reveals a homologous
                  block structure in the promoter regions
JOURNAL           Genome Res. 14 (9), 1711-1718 (2004)
PUBMED            15342556
COMMENT           Contact: Yutaka Suzuki
                  Department of Virology
                  Institute of Medical Science, University of Tokyo
                  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                  Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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                  /clone="HS105902"
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                  /clone_lib="Sugano cDNA library, small intestine"

ORIGIN
Alignment Scores:
Pred. No.:        27.7      Length:      583
Score:            45.00     Matches:      9
Percent Similarity: 100.0%   Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:      100.0%     Indels:      0
DB:               3         Gaps:         0

US-10-757-745-2_COPY_145_153 (1-9) x BP262103 (1-583)
OY               1 Prokaryotic|lepheng|n|u|v|a| 9

```


DB 367 CCAGATGATATTTCTACAGAGATT 393

RESULT 80
BP262741 583 bp mRNA linear EST 16-SEP-2004

LOCUS BP262741 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION clone HS107919, mRNA sequence.

ACCESSION BP262741

VERSION BP262741.1 GI:52177972

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 583)

AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/clone="HS107919"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:

Pred. No.:	27.7	Length:	583
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BP262741 (1-583)

QY 1 Proasparil11ephelung1ngu1a1 9

DB 303 CCAGATGATATTTCTACAGAGATT 329

RESULT 81
BP319548 583 bp mRNA linear EST 17-SEP-2004

LOCUS BP319548 Sugano cDNA library, pericardium Homo sapiens cDNA clone

DEFINITION PC011128, mRNA sequence.

ACCESSION BP319548

VERSION BP319548.1 GI:52248523

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 583)

AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT Contact: Yutaka Suzuki
Department of Virology

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source 1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PC011128"
/tissue_type="pericardium"
/clone_lib="Sugano cDNA library, pericardium"

ORIGIN

Alignment Scores:

Pred. No.:	27.7	Length:	583
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BP319548 (1-583)

QY 1 Proasparil11ephelung1ngu1a1 9

DB 482 CCAGATGATATTTCTACAGAGATT 508

RESULT 82
BU783229 583 bp mRNA linear EST 11-OCT-2002

LOCUS BU783229 in01a08.y1 Human in01a08 Homo sapiens cDNA clone IMAGE:6123158

DEFINITION 5' similar to TR:095551 O95551 D030M3.3, mRNA sequence.

ACCESSION BU783229

VERSION BU783229.1 GI:23827207

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 583)

AUTHORS Melton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K., Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Maza,M., Page,D., Wylie,T., Martin,J., Bliscain,A., Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarashvili,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Other ESTs: in01a08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40bp from Gibco
High quality sequence stop: 430.

FEATURES
source 1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6123158"
/tissue_type="in01a08"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human in01a08"

/note="Organ: pancreas; Vector: pluescript SK-; Site:1: xhoi; Site:2: EcoRI; Constructed with lambda Zapit system (Stratagene) by Dr. J. Ferrier, in vivo mass-excised to pluescript SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.: 27.7 Length: 583
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BU783229 (1-583)

OY 1 Proapva111ephelenglncluv1 9

DB 431 CCAGATGATATTTCTACAGAAAGTT 457

RESULT 83

LOCUS

BP263059 BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

FEATURES

ORIGIN

Alignment Scores:

Pred. No.: 27.7 Length: 584
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP263059 (1-584)

OY 1 Proapva111ephelenglncluv1 9

DB 356 CCGATGATATTTCTACAGAAAGTT 382

RESULT 84

LOCUS

BP248623 BP248623 Sugano cDNA library, brain Homo sapiens cDNA clone

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

FEATURES

ORIGIN

Alignment Scores:
Pred. No.: 27.7 Length: 584
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP248623 (1-584)

OY 1 Proapva111ephelenglncluv1 9

DB 463 CCGATGATATTTCTACAGAAAGTT 499

RESULT 85

LOCUS

BP236074 BP236074 Sugano cDNA library, coronary artery endothelial cell Homo sapiens cDNA clone HCR06784, mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yszuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..588

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR06784"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_lib="Sugano cDNA library, coronary artery endothelial cell"

ORIGIN

Alignment Scores:
Pred. No.: 28 Length: 588
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP236074 (1-588)

Qy 1 ProaapVal11epheLeuGInGluVal 9
|||||
469 CCAGATGTGATATTCTACAGAGATT 495

Db BP348796
BP348796 588 bp mRNA linear EST 17-SEP-2004
DEFINITION BP348796 Sugano cDNA library, brain Homo sapiens cDNA clone
SZR01880, mRNA sequence.
BP348796
ACCESSION BP348796
VERSION BP348796.1 GI:52278781
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 588)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
JOURNAL Contact: Yutaka Suzuki
PIRMEB Department of Virology
COMMENT Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yszuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..588
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SZR01880"
/tissue_type="brain"
/clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:
Pred. No.: 28 Length: 588
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP348796 (1-588)

Qy 1 ProaapVal11epheLeuGInGluVal 9
|||||
461 CCAGATGTGATATTCTACAGAGATT 487

Db AL703449
AL703449 602 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686G0621.r1.686 (synonym: h1cc3) Homo sapiens cDNA clone
DKFZp686G0621.5, mRNA sequence.
AL703449
ACCESSION AL703449
VERSION AL703449.1 GI:19686804
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 602)
Ansorge,W., Winkner,U., Mewes,W., Weil,B. and Wiemann,S.
EST (Ansorge,W., Winkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories, of the
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp686G0621) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..602
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686G0621"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: h1cc3)"
/note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Alignment Scores:
Pred. No.: 28.7 Length: 602
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AL703449 (1-602)

Qy 1 ProaapVal11epheLeuGInGluVal 9
|||||
434 CCAGATGTGATATTCTACAGAGATT 460

Db CB069952
CB069952 621 bp mRNA linear EST 21-JAN-2003
DEFINITION is1j1e10.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5554035 5'
similar to TR:095551 095551.DJ30M3.3, mRNA sequence.
CB069952
ACCESSION CB069952
VERSION CB069952.1 GI:27814472
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS

1 (bases 1 to 621)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Keestner, K., Lemiska, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Bistain, A., Schmitt, A., Reising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 1811e10.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@ionh.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -400p from Gibco
High quality sequence stop: 476.
Location/Qualifiers

FEATURES
source

1..621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6554035"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_id="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site: 1; NotI; Site 2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size: 1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, Metabolism Div. (Alan Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Alignment Scores:
Pred. No.: 29.7 Length: 621
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CB069952 (1-621)

QY 1 PROApyValillePheleuglGluVal 9

DB 439 CCAGATGTATATTCTACGAGAGTT 465

RESULT 89
BP977971 626 bp mRNA linear EST 22-JAN-2001
LOCUS 602148451f1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4307317 5',
DEFINITION mRNA sequence.
ACCESSION BP977971
KEYWORDS BP977971.1 GI:12345186
SOURCE EST
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 626)
AUTHORS NIH-MGC, <http://mgs.nci.nih.gov/>,
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gsgeob@nci.nih.gov
Tissue Procurement: ATCC/DC/DTP
DNA Library Preparation: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://imgc1177.nci.nih.gov> e column: 14
Plate: LNL1177 row: e
High quality sequence stop: 614.
Location/Qualifiers

FEATURES
source

1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4307317"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_62"
/note="Organ: Skin; Vector: pDNR-LIB (Clontech); Site: 1; SfiI (ggccgacgagc); Site 2: SfiI (ggccatagc); double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCRAGACCGCGCGCGCGCGCGCATG-AT(30)BN-3' (where B = A, 75 kb (range 0.9-4.0 kb), 15/15 colonies insert size 1.75 kb (range 0.9-4.0 kb). Average contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Alignment Scores:
Pred. No.: 30 Length: 626
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP977971 (1-626)

QY 1 PROApyValillePheleuglGluVal 9

DB 447 CCAGATGTATATTCTACGAGAGTT 473

RESULT 90

CB157906

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 634)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.W., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52, Boseun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: F column: 06
High quality sequence stop: 634.
Location/Qualifiers

FEATURES

source

```
1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="U18POOL1n1-5-P06"
/cell_line="SNU-354-Cho-CK+Choi-CK+HLK-3"
/lab_host="Top10"
/clone_lib="U18POOL1n1"
/note="Organ: Liver; Vector: pRTT3-Pac; Site 1: EcoRI;
Site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lemmon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."
```

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
30.5	45.00	634	9	0	0	0	0
Percent Similarity:	100.0%						
Best Local Similarity:	100.0%						
Query Match:	100.0%						

US-10-757-745-2_COPY_145_153 (1-9) x CB157906 (1-634)

Qy 1 ProaPvAl1lePhelengIngluval 9
DB 385 CCAGATGCATATTTCTACAGAGATT 411

RESULT 91
CV023369 634 bp mRNA linear EST 20-AUG-2004
LOCUS 288 Full Length cDNA from the Mammalian Gene Collection Homo
DEFINITION sapiens cDNA 5' similar to BC017553, mRNA sequence.
ACCESSION CV023369
VERSION CV023369.1 GI:51481130
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 634)
Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Stimons,B., Segueria,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
Vandenauwe,J., Cusick,M.E., Alcala,V.S., Hill,D.E. and Vidal,M.
Human ORFeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) in press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR primers
FORWARD: ATGGAGTTGGGAGTTGCCTGGA
BACKWARD: TACATATATATCTAAGTTGCACAGAG
Insert length, 634 Std Error: 32.00

Plate: 11008 row: 05 column: F
Seq primer: ACTGCGCTCGTTTACACGCTGCTGACTGGGAAAC
High quality sequence start: 97
High quality sequence stop: 633
POLYA-No.

FEATURES

source

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1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
Collection"
/note="Vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor vector.- Reference : MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"
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ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
30.5	45.00	634	9	0	0	0	0
Percent Similarity:	100.0%						
Best Local Similarity:	100.0%						
Query Match:	100.0%						

US-10-757-745-2_COPY_145_153 (1-9) x CV023369 (1-634)

Qy 1 ProaPvAl1lePhelengIngluval 9
DB 433 CCAGATGCATATTTCTACAGAGATT 459

RESULT 92
BI333830 644 bp mRNA linear EST 30-JUL-2001
LOCUS 602999339P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141577 5',
DEFINITION mRNA sequence.
ACCESSION BI333830
VERSION BI333830.1 GI:15018487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 644)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLM at:
http://image.llnl.gov
Plate: LLM11348 row: n column: 10
High quality sequence stop: 531.
Location/Qualifiers

FEATURES

source

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1..644
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5141577"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
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SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 657)

TITLE Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Flak, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

JOURNAL Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation

COMMENT Nat. Biotechnol. 22 (6), 707-716 (2004)

FEATURES 15146197

source Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 657 Std Error: 0.00.
Location/Qualifiers

ORIGIN 1..657

Alignment Scores:

Pred. No.:	31.7	Length:	657
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CN298920 (1-657)

Qy 1 Proaspvali1ephelengingluval 9

DB 389 CCAGATGATATTTCTACAGAGATT 415

RESULT 96

LOCUS CN791432. 674 bp mRNA linear EST 26-MAY-2004

DEFINITION 4126159 BARC 8BOV Bos taurus cDNA clone 8BOV_42B11 5', mRNA

ACCESSION CN791432

VERSION CN791432.1 GI:47687412

KEYWORDS EST.

SOURCE Bos taurus (cow).

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

AUTHORS 1 (bases 1 to 674)

TITLE Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.

JOURNAL Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle

COMMENT Unpublished (2004)

FEATURES Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604

FEATURES Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov

source Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt '- -trim fasta. Vector identified by cross match using options -mismatch 12 -mismatch 18

Seg primer: CCTATTAGTGACACTATAGAC

High quality sequence stop: 674.

Location/Qualifiers 1..674

ORIGIN 1..674

Alignment Scores:

Pred. No.:	32.7	Length:	674
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CN791432 (1-674)

Qy 1 Proaspvali1ephelengingluval 9

DB 340 CCTGATGATATTTCTACAGAGATC 366

RESULT 97

LOCUS BG719113 678 bp mRNA linear EST 08-MAY-2001

DEFINITION 602699045F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831186 5', mRNA sequence.

ACCESSION BG719113

VERSION BG719113.1 GI:13998300

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 678)

TITLE NIH-MGC http://mgs.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

FEATURES Contact: Robert Strusberg, Ph.D.
Email: cgep@remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshitsuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLM10753 row: 1 column: 11
High quality sequence stop: 672.
Location/Qualifiers

```

source
1. .678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4831186"
/lab_host="DH10B"
/clone_lib="NIH MGC 97"
/notes="Organ: testis; Vector: plasmidscript (modified
plasmidscript KS+); Site 1: BamHI; Site 2: SalI; XhoI
(gcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTT-3', size-selected for average
insert size 2.2 kb and normalized to R0.5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carnini, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes Of Health). Note: this is
a NIH_MGC library."

```

Alignment Scores:	32.9	Length:	678
Pred. No.:	13.0	Match:	9
Score:	45.0	Mismatches:	5
Score Similarity:	100.0%	Mismatches %:	0
Best Local Similarity:	100.0%	Indels:	0
Query Match:	100.0%	Gaps:	0
DB:	2		

Oy	1	ProAspValIlePheLeuGlnIuVal	9
Db	455	CCAGATGTGATATTCTACAGGAAGTT	481

RESULT 98	LOCUS	DEFINITION	ACCSSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CK952220	CK952220	4091.710 BARC 10BOV Bos taurus cDNA clone 10BOV29_F21 5', mRNA sequence.	CK952220	CK952220.1	GI:4546600	EST.	Bos taurus
		680 bp mRNA linear					Bos taurus (cow)

REFERENCE
Sonegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
G.P., Boase, S., Rubenfield, M. and Gabarre, L.C.
1 (bases 1 to 680)
TITLE
Production of EST from cDNA libraries derived from immunologically
activated bovine gut
JOURNAL
Unpublished (2004)
COMMENT
Contact: Tad S. Sonegard

JOURNAL COMMENT

Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Edg 200 Rm2a BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tad@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options "-trim_al" "-trim.fasta. Vector identified
by cross_match using options "-mismatch 12 -minscore 18
Plate: 29 row: F column: 21
Seq primer: CCCAGTCACGACGTTGTAACG
High quality sequence stop: 680.

```

FEATURES
source
location/Qualifiers
1..680
/organism="Bos taurus"
/mol_type="rRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="10BOV29_F21"
/sex="Male"

```

```

/tissue_type="Pooled"
//stage="Multiple"
/lab_host="DHIO T1 phage resistant"
/clone_id="BARC 10BOV"
/ncore="Organ: Small Intestine; Vector: pigen-1; Site: 1
ECORX; Site: 2; NotI; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and
distal ileums of 14 day old calves, proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"

```

Alignment Scores:	
Pred. No.:	33
Score:	43.00
Best Similarity:	45.00
Best Local Similarity:	100.00
Query Match:	100.00
DB:	7
US-10-757-745-2_COPY_145_153	(1-9) × CK952220 (1-680)
	Length: 680
	Matches: 3
	Matched: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

Qy	1	ProAspValIlePheLeuGlnIuVal	9
Db	76	CCTGATGTGATATTCTACAGGAAGTC	102

RESULT	99
CN789157	
LOCUS	
DEFINITION	CN789157 683 bp mRNA linear EST 26-MAY-2004
ACCESSION	4133581 BARC 8BOV Bos taurus cDNA clone 8BOV_37N03 5' mRNA
VERSION	CN789157 sequence.
KEYWORDS	CN789157.1 GI:47685137
SOURCE	EST.
ORGANISM	Bos taurus (cow)
	Bos taurus

REFERENCE	1 (bases 1 to 603)
AUTHORS	Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.
TITLE	Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL	Unpublished (2004)
COMMENT	Contact: Richard G. Baumann

Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-BAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rburnham@anri.barc.usda.gov
Single base sequencing. Bases called and trimmed with phred
0.000925 using options '-trim alt '-trim fasta. Vector identified
by cross_match using options '-mismatch 12 -minscore 18
Plate: 37 row: N column: 03
Seq primer: CCCTATTATGCTGACCTTATGAC
High quality sequence step: 683.

```

FEATURES
  source
    location/Qualifiers
      1..683
        organism="Bos taurus"
        mol_type="mRNA"
        strain="Holstein"
        db_xref="taxon:9913"
        clone="ABOV_37N03"
        sex="Female"
        tissue_type="Epithelial, Muscle"
        dev_stage="lactating, Neonatal"
        lab_host="DH10B Tona"
        clone_1lb="BARC ABOV"
        note="Organ: Intestine; Vector: pCMVSPORT6.1; Site_1:
        Nof1; Site_2: EcorI; Normalized cow cDNA intestinal mRNA
        library in pCMVSPORT6.1, constructed from equimolar mRNA

```


ORIGIN pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 lactating, proximal duodenum, jejunum, distal ileum, colon, 1/5 neonatal, proximal duodenum, jejunum, distal ileum"

Alignment Scores:

Pred. No.: 33.1 Length: 683
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN789157 (1-683)

Qy 1 Proaspvalillepheleungingluval 9
DB 334 CCTGATGATATTTCTACAGAAATC 360

RESULT 100

CK981492 685 bp mRNA linear EST 16-MAR-2004
LOCUS 4114013 BARC 9BOV Bos taurus cDNA clone 9BOV43_H04 5', mRNA
DEFINITION sequence.

ACCESSION CK981492.1 GI:45499472
VERSION CK981492.1
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 685)
AUTHORS Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
~TITLE Production of EST from cDNA libraries derived from immunologically activated bovine gut

JOURNAL COMMENT

Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt "-trim fasta. Vector identified by cross match using options -mismatch 12 -mismatch 12
Plate: 43 row: H column: 04
Seq primer: CCCAGTCACGACCTGTAAACG
High quality sequence stop: 685.
Location/Qualifiers

FEATURES

1..685
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="9BOV43_H04"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_1lb="BARC 9BOV"
/note="Organ: Abomasum; Vector: pagen-1; Site 1: EcoRV; Site 2: NotI; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers. Exposure to *Ostreia* gastritis was initiated at 15 weeks of age. fundic and pyloric abomasum"

ORIGIN

Alignment Scores:
Pred. No.: 33.3 Length: 685

Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CK981492 (1-685)

Qy 1 Proaspvalillepheleungingluval 9
DB 127 CCTGATGATATTTCTACAGAAATC 153

RESULT 101

CR767236 701 bp mRNA linear EST 23-SEP-2004
LOCUS DKFZP469E1236 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DEFINITION DKFZP469E1236 5', mRNA sequence.
CR767236
VERSION CR767236.1 GI:52609173
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pongo.
REFERENCE 1 (bases 1 to 701)
AUTHORS Ansoorge, W., Krieger, S., Regiert, T., Rittmüller, C., Schwager, B., Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
Pongo pygmaeus mRNA (Ansoorge, W., Krieger, S., Regiert, T., et al.)
Unpublished (2004)
Contact: MIPS

~TITLE Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZP469E1236
Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

1..701
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZP469E1236"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="469 (synonym: pkid1)"
/note="Vector: pSPORT1_Sfi; Site 1: SfiIa; Site 2: SfiIb"

ORIGIN

Alignment Scores:
Pred. No.: 34.1 Length: 701
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR767236 (1-701)

Qy 1 Proaspvalillepheleungingluval 9
DB 361 CCAGATGATATTTCTACAGAAATT 387

RESULT 102

B1334620 704 bp mRNA linear EST 30-JUL-2001
LOCUS 602998939P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE5141193 5', mRNA sequence.

```

ACCESSION   B1334820
VERSION     B1334820.1
KEYWORDS    GI:15019477
SOURCE      EST.
ORGANISM    Homo sapiens (human)

REFERENCE   1 (bases 1 to 704)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgsabbs-remail.nih.gov
            CDNA Library Preparation: Life Technologies, Inc.
            Tissue Procurement: ATCC
            CDNA Library Arrayed by: Incyte Genomics, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILMIL at:
            http://image.llnl.gov
            Plate: L1AM11347 row: n ccolumn: 10
            High quality sequence stop: 704.
            Location/Qualifiers
                1..704
                /organism="Homo sapiens"
                /mol_type="RNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5141193"
                /tissue_type="cervical carcinoma cell line"
                /lab_host="DH10B"
                /clone_1ib="NIH MGC.12"
                /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NCI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.4 kb. Library prepared by Life
                Technologies."

ORIGIN
Alignment Scores:
Pred No.:      34.3      Length:      704
Score:         45.00     Matches:      9
Percent Similarity: 100.0%      Mismatches:  0
Best Local Similarity: 100.0%      Indels:      0
Query Match:   100.0%      Gaps:        0
DB:            3

US-10-757-745-2_COPY_145_153 (1-9) x B1334820 (1-704)
QY      1 ProaapValIIlePhelaungInGuaV 9
Db      421 CCGAGTGGCAATTTCTACAGGAGT 447

RESULT 103
B0661472 710 bp mRNA linear EST 30-SEP-2002
LOCUS     B0661472
DEFINITION c172d11.z1 Hembase; Erythroid Precursor Cells (LCB:cl library) Homo
sapiens CDNA clone c172d11 5', mRNA sequence.
ACCESSION B0661472
VERSION   B0661472.1
KEYWORDS  GI:23373654
SOURCE    EST.
ORGANISM  Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 710)
Gubin,A.N., Lee,J.T., Bouffard G.G. and Miller,J.L.
Unpublished (2002)
Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD

```

20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jmf@nih.gov
The 'cl' library was constructed by Alexander Gubin, Ph.D. in the
Laboratory of Chemical Biology, NIDDK, NIH. DNA sequencing and/or
analyses by National Institutes of Health Intramural Sequencing
Center (NISC). More information available at:
http://hembase.nidk.nih.gov
Plate: 72 row: d column: 11
Seq primer: 5' lambda2-1b1b2 Sequencing Primer.
Location/Qualifiers
1. 710
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c172d11"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Precursor Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Precursor erythroblasts; GPA+"
/lab_host="DH5alpha"
/clone_1b="Hembase; Erythroid Precursor Cells (LCB:c1
library)"
/note="Organ: blood; Vector: pTriplEx2. Site 1: 5f11;
Site 2: 5f11; A complementary DNA (cDNA) library from
human erythroid precursor cells was constructed using
SMART PCR (polymerase chain reaction) cDNA library
Construction Kit (Clontech, Palo Alto, CA) according to
the manufacturer's directions, but with slight
modifications. Briefly, reverse transcription was
performed in the presence of 1 umol/l peptide nucleic acid
(PNA) oligos
(N-terminal) -biotin-GTC-CAC-CCC-ANG-CTT-G-(C-terminal) and
(N-terminal) -biotin-C/T/C/T-GAA-GTT-CTC-AGG-A-(C-terminal)
. Synthesized cDNA was digested with 5f11 and
size-selected on a 1% agarose gel (1800bp). Large-scale
sequencing of the library was performed by the NIH
Intramural Sequencing Center (NISC).
Http://www.nisc.nih.gov/."

ALIGNMENT SCORES:
Pred. No.: 34.6 Length: 710
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 9
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BU661472 (1-710)
1 ProAaPValIIlePheLeuGInGInVal 9
DB 349 CCAGATGATGATATTTCTACACGAGAGATT 375

RESULT 104
LOCUS CN298923 711 bp mRNA linear EST 16-MAY-2004
DEFINITION CN298923 17000600002122 GRN_PPREHP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN298923
VERSION CN298923.1 GI:47315337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 711)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muzage, J., Pisk, G. J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandatam, R.,

TITLE
Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation.
JOURNAL
Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED
15146197
COMMENT
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 711 Std Error: 0.00.
Location/Qualifiers
1..711
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_1lb="GRN_PREHEP"
/note="oligo dt primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN
Alignment Scores:
Pred. No.: 34.7 Length: 711
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN298923 (1-711)

QY
1 ProAapValIIlePheLeuGInGluVal 9
|||||

Db
398 CCAGATGATATTTCTACAGAGAGTT 424
|||||

RESULT 105
CN298922 729 bp mRNA linear EST 16-MAY-2004
LOCUS 1700060007717 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN298922
ACCESSION CN298922
VERSION CN298922.1 GI:47315336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 729)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_1lb="GRN_PREHEP"
/note="oligo dt primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN
Alignment Scores:
Pred. No.: 35.7 Length: 729
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN298924 (1-729)

QY
1 ProAapValIIlePheLeuGInGluVal 9
|||||

Db
425 CCAGATGATATTTCTACAGAGAGTT 451
|||||

RESULT 106
CN298924 729 bp mRNA linear EST 16-MAY-2004
LOCUS 17000424496911 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN298924
ACCESSION CN298924
VERSION CN298924.1 GI:47315338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 729)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_1lb="GRN_ES"
/note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Alignment Scores:
Pred. No.: 35.7 Length: 729
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN298924 (1-729)

QY 1 Proaspyvalli1lephleugIngluval 9
 Db 367 CCAGATGTGATTTCTACAGAGATT 393

RESULT 107
 CX760857 731 bp mRNA linear EST 24-JAN-2005
 LOCUS DKEZp4681522_r1_468 (synonym: phrt1) Pongo pygmaeus cDNA clone
 DEFINITION DKEZp4681522 5', mRNA sequence.
 ACCESSION CX760857 GI:56057513
 VERSION CX760857.1 GI:56057513
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo
 1 (bases 1 to 731)
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLES Unpublished (1999)
 JOURNAL
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 National Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: ggerhard@mail.nih.gov
 Issue Description: Meri Ripio
 cDNA Library Preparation: Express Genomics
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov:8080/plate.html
 Plate: 15944 Row: D Column: 14
 High quality sequence stop: 574.
 Location/Qualifiers
 1..731
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:7783600"
 /tissue_type="pluripotent cell line derived from
 blastocyst inner cell mass"
 /lab_host="DH10B TONa"
 /clone_id="NIH-MGC 281"
 /notes="Organ: Blastocyst; Vector: pExpress-1; Site 1:
 EcoRV, Site 2: NotI; RNA obtained from pluripotent cell
 line derived from blastocyst inner cell mass (cell line
 HSE-6, NIH Registry designation UC06. Positive for OCT4
 expression by RT-PCR, positive for SSEA-3, SSEA-4,
 TRA-1-81, TRA-1-60 by immunofluorescence. Negative for
 SSEA-1 by immunofluorescence. Passage 62. cDNA was primed
 using oligo-dT primers:
 5'-pGACTGCTTCATGTCGAGCGCGCC(T)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
 kb resulted in an average insert size of 2.0 kb. This
 primary library is normalized (non-normalized primary
 library is NIH-MGC 280) and was constructed by Express
 Genomics (Frederick, MD). Note: this is a Mammalian Gene
 Collection library."

ORIGIN
 Alignment Scores:
 Pred. No.: 35.8 Length: 731
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 8 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CX760857 (1-731)
 QY 1 Proaspyvalli1lephleugIngluval 9

Db 437 CCAGATGTGATTTCTACAGAGATT 463

RESULT 108
 CR791801 739 bp mRNA linear EST 01-OCT-2004
 LOCUS DKEZp4681522_r1_468 (synonym: phrt1) Pongo pygmaeus cDNA clone
 DEFINITION DKEZp4681522 5', mRNA sequence.
 ACCESSION CR791801
 VERSION CR791801.1 GI:53710641
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Pongo
 1 (bases 1 to 739)
 REFERENCE Outenweilder,B.; Obermaier,B.; Deutschenbaur,S.; Schaipp,A.;
 Mewes,H.W.; Weil,B.; Amlid,C.; Osainger,A.; Fobo,G.; Han,M. and
 Wiemann,S.
 Pongo pygmaeus mRNA (Outenweilder,B., Obermaier,B.,
 Deutschenbaur,S., et al.)
 Unpublished (2004)
 CONTACT: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ),
 Email s.wiemann@dkfz-heidelberg.de, sequenced by Medigenomix
 (Martinsried/Germany) within the cDNA sequencing consortium of the
 German Genome Project. This clone (DKEZp4681522) is available at
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
 Berlin, Germany. Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneid=DKEZp4681522
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna.
 Location/Qualifiers
 1..739
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKEZp4681522"
 /tissue_type="heart"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_id="468 (synonym: phrt1)"
 /note="Vector: pSport1_Sfi; Site_1: Sfi1A; Site_2: Sfi1B"

ORIGIN
 Alignment Scores:
 Pred. No.: 36.3 Length: 739
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR791801 (1-739)
 QY 1 Proaspyvalli1lephleugIngluval 9
 Db 451 CCAGATGTGATTTCTACAGAGATT 477

RESULT 109
 CR767800 749 bp mRNA linear EST 23-SEP-2004
 LOCUS DKEZp4690058_r1_469 (synonym: pkidl) Pongo pygmaeus cDNA clone
 DEFINITION DKEZp4690058 5', mRNA sequence.
 ACCESSION CR767800
 VERSION CR767800.1 GI:52610302
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pongo.
1 (bases 1 to 749)
Ostenwaelder, B., Obermaier, B., Deutschenbaur, S., Schallp, A., Mewes, H.W., Weill, B., Amdt, C., Osanger, A., Fodor, G., Han, M. and Wiemann, S.

TITLE

Pongo pygmaeus mRNA (Ostenwaelder, B., Obermaier, B., Deutschenbaur, S., et al.)

JOURNAL
COMMENT

Unpublished (2004)
Contact: MIPS

FEATURES

Location/Qualifiers
1..749
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469C058"
/cissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_11b="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Alignment Scores:

Pred. No.:	36.8	Length:	749
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CR767800 (1-749)

QY 1 ProaPVal111epheugInguVal 9
|||||
DB 46 CCAGATGATATTTCTACAGAGTT 72

RESULT 110

BI181461 750 bp mRNA linear EST 10-JUL-2001
LOCUS UNL-P-FN-ak-a-12-0-UNL.81 UNL-P-FN Sus scrofa cDNA clone
DEFINITION UNL-P-FN-ak-a-12-0-UNL 3', mRNA sequence.
ACCESSION BI181461
VERSION BI181461.1 GI:14655870
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

AUTHORS

TITLES

JOURNAL

COMMENT

1 (bases 1 to 750)
Caetano, A.R., Johnson, R.K. and Pomp, D.
Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles
Mamm. Genome 14 (1), 65-70 (2003)
12532269
Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA

Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dt track not found, Not 1 site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
POLY(A)=No.

FEATURES

source

Location/Qualifiers
1..750
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="University of Nebraska, Lincoln Swine Selection
lines"

/db_xref="taxon:9623"
/clone="UNL-P-FN-ak-a-12-0-UNL"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_11b="UNL-P-FN"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dt track. The library was constructed as described
by Bonaldi, Lennon and Soares, Genome Research 6:
791-806, 1996.
TAG_SEQ=None found"

ORIGIN

Alignment Scores:

Pred. No.:	36.9	Length:	750
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BI181461 (1-750)

QY 1 ProaPVal111epheugInguVal 9
|||||
DB 447 CCAGATGATATTTCTACAGAGTT 473

RESULT 111

BF243927 751 bp mRNA linear EST 14-NOV-2000
LOCUS 601877278F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105866 5',
DEFINITION mRNA sequence.
ACCESSION BF243927
VERSION BF243927.1 GI:1157869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homiidae; Homo.

REFERENCE

AUTHORS

TITLES

JOURNAL

COMMENT

1 (bases 1 to 751)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
<http://image.llnl.gov>
Plate: L10C984 row: k column: 19

High quality sequence stop: 533.
Location/Qualifiers
1..751
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4105866"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 35"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccatcgcc); Site 2: SfiI (ggccatcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCAGCATG-AT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Alignment Scores:
Pred. No.: 36.9 Length: 751
Score: 45.00 Matches: 9
Percent Similarity: 100.04 Conservative: 0
Best Local Similarity: 100.04 Mismatches: 0
Query Match: 100.04 Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF243927 (1-751)

QY 1 ProapvAl1lephelengInguva1 9
|||||
422 CCAGATGTGATATTCTACGAGAGTT 448

RESULT 112
AUI39147 752 bp mRNA linear EST 02-AUG-2002
LOCUS AUI39147 PLACE1 Homo sapiens cDNA clone PLACE1010031 5', mRNA
DEFINITION
Sequence:
ACCESSION AUI39147
VERSION AUI39147.1 GI:11000668
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
Homidates 1 to 752)
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y., Yamamoto.T., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and Iwagui.T.
HRI human cDNA project
Unpublished (2000)
Contract: Takao Isegai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute, cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute
Location/Qualifiers
1..752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source

/clone="PLACE1010031"
/tissue_type="Placenta"
/clone_lib="PLACE1"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:
Pred. No.: 37 Length: 752
Score: 45.00 Matches: 9
Percent Similarity: 100.04 Conservative: 0
Best Local Similarity: 100.04 Mismatches: 0
Query Match: 100.04 Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AUI39147 (1-752)

QY 1 ProapvAl1lephelengInguva1 9
|||||
433 CCAGATGTGATATTCTACGAGAGTT 459

RESULT 113
BI760756 757 bp mRNA linear EST 25-SEP-2001
LOCUS BI760756 603044763PL NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185334 5',
DEFINITION
mRNA sequence.
ACCESSION BI760756
VERSION BI760756.1 GI:15752334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
Homidates 1 to 757)
1 (bases 1 to 757)
NIH-MGC Inc./p/mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cga@hri-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11462 row: m column: 15
High quality sequence start: 6
High quality sequence stop: 755.
Location/Qualifiers
1..757
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5185334"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled (human, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed)); RNA source anonymous pool of 46 yo male kidney, and pool of 2 female, 71 yo male colon, 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C-Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 37.3 Length: 757
Score: 45.00 Matches: 9

Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B160756 (1-757)

QY 1 Proaapvalli1ephelengingluval 9
 DB 340 CCAGATGATATTTCTACAGAGATT 366

RESULT 114

B1258848

LOCUS 767 bp mRNA linear EST 17-JUL-2001
 DEFINITION 60256963F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109303 5',
 mRNA sequence.

ACCESSION B1258848
 VERSION B1258848
 KEYWORDS GI:14815606
 SOURCE EST.

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 767)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS Unpublished (1999)
 TITLE
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov

FEATURES

source
 Location/Qualifiers
 1..767
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5109303"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 Plate: L14M1264 row: m column: 16
 High quality sequence stop: 758.

FEATURES

source
 Location/Qualifiers
 1..767
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5109303"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

ORIGIN

Alignment Scores:
 Pred. No.: 37.8 Length: 767
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B158848 (1-767)

QY 1 Proaapvalli1ephelengingluval 9
 DB 370 CCAGATGATATTTCTACAGAGATT 396

RESULT 115

BG391295

LOCUS 770 bp mRNA linear EST 12-MAR-2001
 DEFINITION 602417344F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4536634 5',
 mRNA sequence.

ACCESSION BG391295
 VERSION BG391295.1 GI:13284743
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov

ACCESSION BG391295
 VERSION BG391295.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov

ACCESSION BG391295
 VERSION BG391295.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov

ACCESSION BG391295
 VERSION BG391295.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov

ACCESSION BG391295
 VERSION BG391295.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov

ACCESSION BG391295
 VERSION BG391295.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov

CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLCN1474 row: a column: 02
High quality sequence stop: 668.
Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:466653"
/life_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/notes="Organ: prostate; Vector: pDMR-11B (Clontech);
Site_1: SfiI (ggcgctcgcc); Site_2: SfiI
(ggcattatggcc); Double-stranded cDNA was
cloned in cloning as follows: 5' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-
dT(30)BN-3' (where B = A, C, or G and N =
A, C, G, or T). Average insert size 1.5
kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was
enriched for full-length clones and
was constructed by Clontech Laboratories
(Palo Alto, CA). Note: this is a NIH_MGC
library."
```

ORIGIN

Alignment Scores:

Pred. No.:	38	Length:	770
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG498689 (1-770)

QY 1 ProaapValIlePheLeuGingJuva1 9
DB 17 CCAGATGATATTTCTACAGAAATT 43

RESULT 117

BI754101 774 bp mRNA linear EST 25-SEP-2001
LOCUS 603027659P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197838 5',
DEFINITION mRNA sequence.
ACCESSION BI754101.1 GI:15745679
VERSION BI754101.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLCN1495 row: f column: 15
High quality sequence stop: 756.

FEATURES

source

Location/Qualifiers
1. 774
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5197838"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/notes="Organ: brain; Vector: pCMV-SPORT6, Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	38.2	Length:	774
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BI754101 (1-774)

QY 1 ProaapValIlePheLeuGingJuva1 9
DB 492 CCAGATGATATTTCTACAGAAATT 518

RESULT 118

BX374579 780 bp mRNA linear EST 27-APR-2004
LOCUS BX374579 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DB007YB11 5-PRIME, mRNA sequence.
ACCESSION BX374579
VERSION BX374579.2 GI:46618956
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS L.I.W.B., Gruber, C., Jesse, J., and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30452317.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdnas/CS0DB007CN060P1ec=3474.r>.

FEATURES

source

```
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB007YB11"
/life_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
```


digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ALIGNMENT SCORES:

Pred. No.:	38.6	Length:	780
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX374579 (1-780)

QY 1 Proasparvallephelengingluval 9
DB 445 CCAGATGATATTTCTACAGAGATT 471

RESULT 119

LOCUS BX365835 783 bp mRNA linear EST 08-APR-2004
DEFINITION BX365835 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
ACCESSION CDNA clone CSODB007YB11 5-PRIME, mRNA sequence.
VERSION BX365835
KEYWORDS BX365835.2 GI:46288859
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 783)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30370946.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of invitrogen. This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSIDB002ZF03P1c=3474.r.

FEATURES

source Location/Qualifiers
1..783
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODB007YB11"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_1ib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	38.7	Length:	783
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX365835 (1-783)

QY 1 Proasparvallephelengingluval 9

DB 445 CCAGATGATATTTCTACAGAGATT 471

RESULT 120

LOCUS BG719977 786 bp mRNA linear EST 08-MAY-2001
DEFINITION 60269135F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4823432 5', mRNA sequence.
ACCESSION BG719977
VERSION BG719977.1 GI:13999164
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 786)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshitaki and Piero Carninci (RIKEN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILN at:
http://image.llnl.gov
Place: LLM10733 row: f column: 09
High quality sequence stop: 784.
Location/Qualifiers
1..786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4823432"
/lab_host="DH10B"
/clone_1ib="NIH MGC 97"
/note="Organ: testis; Vector: BluescriptR (modified pBluescript KS+); Site 1: BamHI, Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

FEATURES

source Location/Qualifiers
1..786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4823432"
/lab_host="DH10B"
/clone_1ib="NIH MGC 97"
/note="Organ: testis; Vector: BluescriptR (modified pBluescript KS+); Site 1: BamHI, Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	38.9	Length:	786
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG719977 (1-786)

QY 1 Proasparvallephelengingluval 9

DB 578 CCAGATGATATTTCTACAGAGATT 604

RESULT 121

LOCUS BG533717 793 bp mRNA linear EST 03-APR-2001
DEFINITION 602562373F1 NIH_MGC_76 Homo sapiens CDNA clone IMAGE:4700059 5', mRNA sequence.
ACCESSION BG533717
VERSION BG533717.1 GI:13525257

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov a column: 20
Plate: LNCM1533 row: a column: 20
High quality sequence stop: 666.
Location/Qualifiers
1..793
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_name="MGC700059"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 76"
/note="Organ. liver. Vector: pDMR-LIB (Clontech); Site 1:
still (ggcgccgcggcc); Site 2: still (ggccattatggcc); 5' and
3' adaptor 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGACGCCGCGAATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:
39.3	793	9
Score: 45.00	Conservative: 0	
Percent Similarity: 100.0%	Mismatches: 0	
Best Local Similarity: 100.0%	Indels: 0	
Query Match: 2	Gaps: 0	

US-10-757-745-2_COPY_145_153 (1-9) x BG53J17 (1-793)

OY 1 ProaPVal11lePhelauGIngluVal 9

DB 289 CCAGATGATATTTCTACAGAAATT 315

RESULT 122

LOCUS DN122208 798 bp mRNA linear EST 15-FEB-2005

DEFINITION 1122287 MARC 4P10 Sus scrofa cDNA 5', mRNA sequence.

ACCESSION DN122208.1 GI:59816487

VERSION

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 798)
AUTHORS Smith, R.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Kohneman, D.J., Wray, J.E. and Keale, J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)

COMMENT Contact: Smith RPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alo option. Vector identified with
cross_match v0.990329.
Plate: HHY8024 row: L column: 17
Seq primer: GTAAATGACATCTCATATGGG.
Location/Qualifiers
1..798
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9923"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P10"
/note="Vector: pCDNA3.1, Site 1: EcoRI, Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:
39.6	798	9
Score: 45.00	Conservative: 0	
Percent Similarity: 100.0%	Mismatches: 0	
Best Local Similarity: 100.0%	Indels: 0	
Query Match: 8	Gaps: 0	

US-10-757-745-2_COPY_145_153 (1-9) x DN122208 (1-798)

OY 1 ProaPVal11lePhelauGIngluVal 9

DB 453 CCAGATGATATTTCTACAGAAATT 479

RESULT 123

LOCUS CX756424 799 bp mRNA linear EST 24-JAN-2005

DEFINITION AGENCOURT_41337854 NIH_MGC_281 Homo sapiens cDNA clone

ACCESSION CX756424

VERSION CX756424.1 GI:58053080

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Euarchontoglires; Primates; Catherhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 799)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Geierhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Meti Flipo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov a column: 21
Plate: LNCM15934 row: C column: 21
High quality sequence stop: 579.
Location/Qualifiers
1..799
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:7779791"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 281"
/note="Organ: Blastocyst; Vector: pExpress-1; Site 1:
ECORV; Site 2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSP-6, NIH Registry designation UC06. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. cDNA was primed
using oligo-dT primer:
5'-pGACTGATCTAGATCGACGAGCGCCGCC(7)25-3' and cloned into
the pECORV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 2.0 kb. This
primary library is normalized (non-normalized primary
library is NIH_MGC_280) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."

ORIGIN

Alignment Scores:
Pred. No.: 39.6 Length: 799
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CX756424 (1-799)

Qy 1 Proaspva111ephelenginglva1 9
Db 450 CCAGATGATATTTCTACAGAGATT 476

RESULT 124

LOCUS CX166335 810 bp mRNA linear EST 23-DEC-2004
DEFINITION HES2_39_B09.g1_A035 NIH MGC 258 Homo sapiens cDNA clone
IMAGE:7469923 5', mRNA sequence.

ACCESSION CX166335
VERSION CX166335.1 GI:56796415

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 810)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabbs-remail.nih.gov

Tissue Procurement: BresaGen, Inc.

cDNA Library Preparation: Express Genomics, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

University of Georgia

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:

<http://image.llnl.gov>

Plate: L14M15771 row: d column: 17

Seg primer: JENREV (CAGGAACACCTATGACC)

High quality sequence stop: 810.

Location/Qualifiers
1..810
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7469923"
/sex="male"
/tissue_type="human embryonic stem cells differentiated to
an early endodermal cell type"
/cell_type="human embryonic stem cells"
/clone_lib="B601"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH MGC 258"
/note="Vector: pExpress-1; Site 1: NotI; Site 2: ECORV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is B601. Positive for
GATA4, Mxi1, Msx1, HNF4alpha expression; negative for AFP
expression. Passage number 40. cDNA primed using oligo-dT
primer: 5'-pGACTGATCTAGATCGACGAGCGCCGCC(7)25-3' and
cloned into the pECORV/NotI sites of pExpress-1. This
primary library is non-normalized (normalized primary
library is NIH_MGC 259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."

ORIGIN

Alignment Scores:
Pred. No.: 40.3 Length: 810
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CX166335 (1-810)

Qy 1 Proaspva111ephelenginglva1 9
Db 390 CCAGATGATATTTCTACAGAGATT 416

RESULT 125

LOCUS BI908925 838 bp mRNA linear EST 16-OCT-2001
DEFINITION B1908925 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215926 5',
mRNA sequence.

ACCESSION BI908925
VERSION BI908925.1 GI:16172029

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 838)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:

<http://image.llnl.gov>

Plate: L14M1542 row: h column: 07

High quality sequence stop: 773.

Location/Qualifiers
1..838
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5215926"
/issue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 41.8 Length: 838
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1908925 (1-838)

OY 1 Proapevalli11epheleugingluva1 9
DB 434 CCAGTGTGATATTCTACAGAGATT 460

RESULT 126

CR765451 846 bp mRNA linear EST 23-SEP-2004
LOCUS CR765451
DEFINITION DKFZP469E2434 r1 469 (synonym: pk1d1) Pongo pygmaeus CDNA clone
ACCESSION CR765451
VERSION CR765451.1 GI:52605526
KEYWORDS EST
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pongo.
1 (bases 1 to 846)
Ostenwelder, B.; Ostermaier, B.; Deutschenbaur, S.; Schapp, A.;
Mewes, H.W.; Weill, B.; Amid, C.; Oeinger, A.; Fobo, G.; Han, M. and
Wiemann, S.
Pongo pygmaeus mRNA (Ostenwelder, B., Ostermaier, B.,
Deutschenbaur, S., et al.)
Unpublished (2004)
COMMENT MIPS

REFERENCES

1 Ingo Stadler Landstr. 1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email: s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
(Martinsried, Germany). Within the CDNA DKFZP469E2434 is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZP469E2434
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/
location/Qualifiers

1 846
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZP469E2434"
/issue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"

FEATURES

source
1 846
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZP469E2434"
/issue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"

/clone_lib="469 (synonym: pk1d1)"
/note="Vector: pSPORT1_gfi; Site 1: SfiI; Site 2: SfiIb"

ORIGIN

Alignment Scores:
Pred. No.: 42.3 Length: 846
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR765451 (1-846)

OY 1 Proapevalli11epheleugingluva1 9
DB 336 CCAGTGTGATATTCTACAGAGATT 362

RESULT 127

BE784416 853 bp mRNA linear EST 20-OCT-2000
LOCUS BE784416
DEFINITION 601473891r1 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:3876862 5',
mRNA sequence.
ACCESSION BE784416
VERSION BE784416.1 GI:10205614
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 853)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strzemecki, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCD/DPR/Life Technologies, Inc.
CDNA Library Preparation: DCD/DPR/Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E Consortium (LNL)
DNA Sequencing by: Incyte Genomics Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E Consortium/LNL at:
http://image.llnl.gov
Plate: LNA9638 row: e column: 23
High quality sequence stop: 660.
Location/Qualifiers

1 853
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3876862"
/issue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SfiI; Cloned unidirectionally; primer: oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

source
1 853
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3876862"
/issue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SfiI; Cloned unidirectionally; primer: oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 42.7 Length: 853
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BE784416 (1-853)

OY 1 Proapevalli11epheleugingluva1 9
DB 336 CCAGTGTGATATTCTACAGAGATT 362

Db 437 CCAGATGATATTTCTACAGAACTT 463

RESULT 128

LOCUS B1553412 858 bp mRNA linear EST 05-SEP-2001

DEFINITION 603193358F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5264582 5', mRNA sequence.

ACCESSION B1553412

VERSION B1553412.1 GI:15440724

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 858)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLM11667 row: c column: 15
High quality sequence stop: 829.

FEATURES

source location/Qualifiers

1..858

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5264582"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_95"

/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size selected for average insert size 2.5 kb and normalized to R07 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 43

Score: 45.00 Length: 858

Percent Similarity: 100.0% Matches: 9

Best Local Similarity: 100.0% Conservative: 0

Query Match: 100.0% Mismatches: 0

DB: 3 Indels: 0

Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1553412 (1-858)

Qy 1 Proaapvalillepheleugingluval 9

Db 453 CCAGATGATATTTCTACAGAACTT 479

RESULT 129

LOCUS BG740396 870 bp mRNA linear EST 15-MAY-2001

DEFINITION 602834171F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779449 5', mRNA sequence.

ACCESSION BG740396

VERSION BG740396.1 GI:14051049

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 870)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLM10636 row: m column: 18
High quality sequence stop: 826.

FEATURES

source location/Qualifiers

1..870

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4779449"

/lab_host="DH10B (TI phage-resistant)"

/clone_lib="NCI CGAP_Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.: 43.7

Score: 45.00 Length: 870

Percent Similarity: 100.0% Matches: 9

Best Local Similarity: 100.0% Conservative: 0

Query Match: 100.0% Mismatches: 0

DB: 2 Indels: 0

Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG740396 (1-870)

Qy 1 Proaapvalillepheleugingluval 9

Db 344 CCAGATGATATTTCTACAGAACTT 370

RESULT 130

LOCUS BU159911 870 bp mRNA linear EST 04-SEP-2002

DEFINITION AGENCOURT 7933863 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6144208 5', mRNA sequence.

ACCESSION BU159911

VERSION BU159911.1 GI:22673821

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 870)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13468 row: n column: 17
High quality sequence stop: 677.
Location/Qualifiers
1..870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6144208"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	43.7	Length:	870
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BU159911 (1-870)

OY 1 ProaspValllePhelengIngluval 9

DB 368 CCAGATGTGATATTCTACAGAGAGTT 394

RESULT 131

BU169945 883 bp mRNA linear EST 04-SEP-2002

LOCUS AGENCOURT 7913097 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6024760

DEFINITION 5', mRNA sequence.

ACCESSION BU169945

VERSION BU169945.1 GI:22683929

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 883)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cga@ps-remail.nih.gov
Tissue Procurement: DCTD/DIR/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13235 row: n column: 17
High quality sequence stop: 413.
Location/Qualifiers
1..883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:024760"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.8 kb. Library constructed by Life

FEATURES

source

Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	44.4	Length:	883
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BU169945 (1-883)

OY 1 ProaspValllePhelengIngluval 9

DB 313 CCAGATGTGATATTCTACAGAGAGTT 339

RESULT 132

BU179107 883 bp mRNA linear EST 04-SEP-2002

LOCUS AGENCOURT 7984768 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6174958

DEFINITION 5', mRNA sequence.

ACCESSION BU179107

VERSION BU179107.1 GI:22693091

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 883)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cga@ps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13548 row: 0 column: 23
High quality sequence stop: 672.
Location/Qualifiers
1..883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6174958"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.1 kb."

FEATURES

source

RESULT 133
 BX422491 904 bp mRNA linear EST 03-MAY-2004
 LOCUS BX422491 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
 DEFINITION CS0DM007YE11 5-PRIME, mRNA sequence.
 ACCESSION BX422491
 VERSION BX422491
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 904)
 Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30766188.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by life technologies, a
 division of invitrogen.
 This sequence belongs to sequence cluster 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DM007AC06Plc=3474.r.
 Location/Qualifiers
 1..904
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DM007YE11"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_1fb="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

FEATURES
 source
 1..904
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DM007YE11"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_1fb="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 45.6 Length: 904
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BX422491 (1-904)

QY 1 Proaapvalillepheleuglgluval 9
 DB 376 CCAGATGTGATATTCTACAGGAAGTT 402
 RESULT 134
 CD251503 906 bp mRNA linear EST 22-MAY-2003
 LOCUS CD251503
 DEFINITION AGENCOURT_14212105 NIH_MGC_179 Homo sapiens cDNA clone
 IMAGE:30385385 5', mRNA sequence.
 ACCESSION CD251503
 VERSION CD251503.1 GI:310111969
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 906)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@b-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM452 row: f column: 18
 High quality sequence stop: 588.
 Location/Qualifiers
 1..906
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30385385"
 /tissue_type="Plutitary"
 /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
 /clone_1fb="NIH_MGC_179"
 /note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
 (destroyed); Site 2: NotI; Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.1 Kb. Library was
 constructed by (Invitrogen). Note: this is a NIH_MGC
 library."

FEATURES
 source
 1..906
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30385385"
 /tissue_type="Plutitary"
 /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
 /clone_1fb="NIH_MGC_179"
 /note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
 (destroyed); Site 2: NotI; Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.1 Kb. Library was
 constructed by (Invitrogen). Note: this is a NIH_MGC
 library."

ORIGIN

Alignment Scores:
 Pred. No.: 45.7 Length: 906
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 6 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CD251503 (1-906)

QY 1 Proaapvalillepheleuglgluval 9
 DB 474 CCAGATGTGATATTCTACAGGAAGTT 500
 RESULT 135
 BG391213 908 bp mRNA linear EST 12-MAR-2001
 LOCUS BG391213
 DEFINITION 602417244F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:453635 5',
 mRNA sequence.
 ACCESSION BG391213
 VERSION BG391213.1 GI:13284661
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 908)
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@b-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

Page 64

and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics' triicking code 017. Note: (Invitrogen)

Full-
(Inv)

```

Alignment scores:
Accession No.: 45.2
Score: 45.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
US-10-757-745-2_COPY_145_153 (1-9) x BI915865 (1-915)

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?

QY	1	Proaspvaalll	epheLeuGlIngluVal	9
Db	444	CGAGATGTGATATTTCTCAAGAGAGTT		470
RESULT 137				
CN801806		922 bp	mRNA	linear
LOCUS				EST 26-MAY-2006
DEFINITION				IL13M1G1GEN.MCO.37066.Katzke/EMBL Macaca mulatta IL13M1G1GEN.MCO.37066.Katzke/EMBL human

ACCESSION	CN801806	
VERSION	CN801806.1	GI:47697782
KEYWORDS	EST.	
SOURCE	Macaca mulatta (rhesus monkey)	
ORGANISM	Macaca mulatta	

REFERENCE	AUTHORS	TITLE
1 (pages 1 to 922)	Magnus, C.L., Pellin, P.C., Thomas, M.J., Agy, M.B., Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and Iadonato, S.P.	Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human

Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Tel: 2063780400
 Fax: 2063780408
 Email: cmgcnsgen@illumigen.com
 Sequenced on 2004.05.13. 514 Q20 bases.

```

FEATURES
source
location/Qualifiers
1..922
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"

```

```

/ab_xref=/taxon:9384
/ab_xref=abx:15450
/clone_from=abx:15450
/dev_stage="adul"
/lab_host="E. coli SOLR"
/clone_lib="kate_MMB"
/notes="Organi: brain; Vector: uni_zap xr; Site:1: Bscr I;
Site:2: Xho I; Created from StrataGene Zap-CNA synthase
kit (catalog #200400) and Zap-CNA Gispesck rti Gold

```


ORIGIN Cloning Kit (Catalog #200450)"

Alignment Scores:

Pred. No.:	46.6	Length:	922
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG19064 (1-922)

QY 1 Proaapvalillepheleuglncgluval 9
|||||
DB 315 CCAGATGATATTTCTACAGAGATT 341

RESULT 138

LOCUS BG119064 927 bp mRNA linear EST 30-JUN-2001
DEFINITION 602347389F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:444239 5',
mRNA sequence.
ACCESSION BG119064 GI:12612570
VERSION BG119064.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10215 row: a column: 24
High quality sequence stop: 676.

FEATURES

source
1..927
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:444239"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: PCMV-SPORE6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	46.9	Length:	927
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG119064 (1-927)

QY 1 Proaapvalillepheleuglncgluval 9
|||||

DB 265 CCAGATGATATTTCTACAGAGATT 291

RESULT 139

LOCUS BG740339 932 bp mRNA linear EST 15-MAY-2001
DEFINITION 602635289F1 NCI_CGAP_Skin3 Homo sapiens cDNA clone IMAGE:4780318 5',
mRNA sequence.
ACCESSION BG740339
VERSION BG740339.1 GI:14050992
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10639 row: a column: 23
High quality sequence stop: 759.

FEATURES

source
1..932
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4780318"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skin3"
/note="Organ: skin; Vector: PCMV-SPORE6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP library."

ORIGIN

Alignment Scores:

Pred. No.:	47.2	Length:	932
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG740339 (1-932)

QY 1 Proaapvalillepheleuglncgluval 9
|||||
DB 264 CCAGATGATATTTCTACAGAGATT 290

RESULT 140

LOCUS BG541819 937 bp mRNA linear EST 03-APR-2001
DEFINITION 602569712F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694066 5',
mRNA sequence.
ACCESSION BG541819
VERSION BG541819.1 GI:13534052
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10639 row: a column: 23
High quality sequence stop: 759.

Contact: Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
The first strand cDNA was primed with a NotI-oligo(dT) primer. Five pri-
er end enriched, double-stranded cDNA was digested with NotI and cloned
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalised. Library was constructed by Life Technologies, a

```

FEATURES
    source
        Location/Qualifiers
            1..948
                /organism="Homo sapiens"
                /mol_type="RNA"
                /db_xref="taxon:9606"
                /clone="CS0DK007K05"
                /cell_type="HELA CELLS COT 25-NORMALIZED"
                /cell_line="HELA"
                /clone_id="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was

```

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	48.1	Length:	948
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AL555333 (1-948)

QY 1 Proaapvalli1lePheLeugIngluVal 9

DB 452 CCAGATGATGATTTCTACAGGAGTT 478

RESULT 143

LOCUS BX433489 952 bp mRNA linear EST 04-MAY-2004

DEFINITION BX433489 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone

CS0N005YN02 3-PRIME, mRNA sequence.

ACCESSION BX433489

VERSION BX433489.2 GI:47002503

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 952)

Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30775195.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?cs=CS0BA10562D12_CS05372_1&c=3474.r

FEATURES

Location/Qualifiers

1..952

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0N005YN02"

/tissue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_lib="Homo sapiens ADULT BRAIN"

/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.:	48.4	Length:	952
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AL555333 (1-948)

QY 1 Proaapvalli1lePheLeugIngluVal 9

DB 451 CCAGATGATGATTTCTACAGGAGTT 477

RESULT 145

LOCUS CN803230 965 bp mRNA linear EST 26-MAY-2004

DEFINITION ILUMIGEN MCQ_32551 Katze_MBR Macaca mulatta cDNA clone

IBIUM:12605 5' similar to Bases 1 to 965 highly similar to human

US-10-757-745-2_COPY_145_153 (1-9) x BX433489 (1-952)

QY 1 Proaapvalli1lePheLeugIngluVal 9

DB 711 CCAGATGATGATTTCTACAGGAGTT 685

RESULT 144

LOCUS BI161201 959 bp mRNA linear EST 05-JUL-2001

DEFINITION 602865659P1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019639 5',

mRNA sequence.

ACCESSION BI161201

VERSION BI161201.1 GI:14621202

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 959)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L10C1835 row: e column: 16

High quality sequence stop: 551.

Location/Qualifiers

1..959

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5019639"

/tissue_type="epitheloid carcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_42"

/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Site-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	48.8	Length:	959
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BI161201 (1-959)

QY 1 Proaapvalli1lePheLeugIngluVal 9

DB 451 CCAGATGATGATTTCTACAGGAGTT 477

RESULT 145

LOCUS CN803230 965 bp mRNA linear EST 26-MAY-2004

DEFINITION ILUMIGEN MCQ_32551 Katze_MBR Macaca mulatta cDNA clone

IBIUM:12605 5' similar to Bases 1 to 965 highly similar to human

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

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TRAP (Hs.210628), mRNA sequence.
ACCESSION CN803230
VERSION CN803230.1 GI:47699206
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 965)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
TITLE
JOURNAL
PUBMED
COMMENT
Contact: C. Magness
illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.04.02. 780 Q20 bases.
PCR Primers
FORWARD: CCTCTACTTAAGGAAACAAA
BACKWARD: CACTTAGGGGGAATGGGTA
Insert Length: 965 Std Error: 0.00
Plate: CL000288 row: D column: 11
Seq primer: CCTCTACTTAAGGAAACAAA
POLYA=No.
FEATURES
source
location/Qualifiers
1..965
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIDW:12605"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MBR"
/note="Organ: Brain; Vector: Uni-ZAP XR; Site 1: Ecor I;
Site 2: Xho I; Created from StrataGene ZAP-CDNA Synthesis
Kit (catalog #200400) and ZAP-CDNA GigaPack III Gold
Cloning Kit (catalog #200450)"
ORIGIN
Alignment Scores:
Pred. No.: 49.1 Length: 965
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x CN803230 (1-965)
QY 1 PROASPVALIIEPHELEUNGIGUVAL 9
DB 200 CCAGATGTGATATTTCTACAGGAAGTT 226
RESULT 146
LOCUS BM468826 972 bp mRNA linear EST 05-FEB-2002
DEFINITION ACENCOUPT_6445782 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587154
5', mRNA sequence.
ACCESSION BM468826
VERSION BM468826.1 GI:18517868
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 972)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LRAM12356 row: d column: 03
High quality sequence stop: 707.
FEATURES
source
location/Qualifiers
1..972
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5587154"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 49.5 Length: 972
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BM468826 (1-972)
QY 1 PROASPVALIIEPHELEUNGIGUVAL 9
DB 328 CCAGATGTGATATTTCTACAGGAAGTT 354
RESULT 147
LOCUS BX338160 981 bp mRNA linear EST 08-APR-2004
DEFINITION BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1056YC23 5-PRIME, mRNA sequence.
ACCESSION BX338160
VERSION BX338160.2 GI:46283046
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 981)
Li,M.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30345671.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creneau, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer, and cloned
end enriched, double-strand cDNA was digested with NotI, and cloned
into the NotI and EcoRV sites of the pCMVSPORT6 vector. Library
was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?c=CSODI056AB120Pic=3474.r>.

FEATURES

source

Location/Qualifiers

1..981

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI056YC23"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	50.1	Length:	981
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX338160 (1-981)

Qy 1 Proaepvalliepheuglncgluval 9

Db 446 CCAGATGATATTTCTACAGAACTT 472

RESULT 148

LOCUS

BE892886 995 bp mRNA linear EST 20-OCT-2000

DEFINITION

601435730F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920790 5', mRNA sequence.

ACCESSION

BE892886

VERSION

BE892886.1 GI:10353510

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LHM9752 row: 1 column: 07

High quality sequence stop: 573.

Location/Qualifiers

1..995

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3920790"

/tissue_type="melanotic melanoma"

/lab_host="DH108 (phage-resistant)"

/clone_lib="NIH MGC 72"

/note="Organ: Skin; Vector: pCMV-SPORT6, site 1: NotI, site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	50.9	Length:	995
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BE892886 (1-995)

Qy 1 Proaepvalliepheuglncgluval 9

Db 462 CCAGATGATATTTCTACAGAACTT 488

RESULT 149

LOCUS

BX337141 1018 bp mRNA linear EST 07-APR-2004

DEFINITION

BX337141 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI036YJ02 5-PRIME, mRNA sequence.

ACCESSION

BX337141

VERSION

BX337141.2 GI:46271144

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?c=CSODI036B01QP1c=3474.r>.

Location/Qualifiers

1..1018

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI036YJ02"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	52.2	Length:	1018
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX337141 (1-1018)

Qy 1 Proaepvalliepheuglncgluval 9

Db 423 CCAGATGATATTTCTACAGAACTT 449

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

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RESULT 150      BM554324      1035 bp      mRNA      linear      EST 20-FEB-2002
LOCUS          BM554324
DEFINITION     AGENCOCOURT_6546794 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742466
VERSION        BM554324.1
KEYWORDS       5', mRNA sequence.
ACCESSION      BM554324.1
SOURCE         GI:18793827
ORGANISM       Homo sapiens (human)
MIMAT          EST.
MIMAT          Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MIMAT          Mammalia; Euteleostomi; Euteleostomi; Primates; Carnivora;
MIMAT          Homnidae; Homo.
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/
AUTHORS        National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE          Unpublished (1999)
JOURNAL        Contact: Robert Strausberg, Ph.D.
COMMENT        Email: cga@bbs-remail.nih.gov
               Tissue Procurement: Life Technologies, Inc.
               cDNA Library Preparation: Life Technologies, Inc.
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.V.G.E. Consortium/LNL at:
               http://image.llnl.gov
               Plate: LHAM12760 row: k column: 11
               High quality sequence stop: 738.
               Location/Qualifiers
                   1..1035
                       /organism="Homo sapiens"
                       /mol_type="mRNA"
                       /db_xref="taxon:9606"
                       /clone="IMAGE:5742466"
                       /tissue_type="medulla"
                       /lab_host="DH10B"
                       /clone_id="NIH_MGC_119"
                       /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
                       Site 2: EcoRV (destroyed); RNA source: normal medulla from
                       anonymous male age 27. Library is oligo-dT primed and
                       directionally cloned (BCRV site is destroyed upon
                       cloning). Average insert size 1.3 kb, insert size range
                       0.9-3 kb. Library is normalized and enriched for
                       full-length clones and was constructed by C. Gher
                       (Invitrogen). Research Genetics tracking code 013. Note:
                       this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:      53.2      Length:      1035
Score:          45.00     Matches:      3
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    100.0%   Indels:      0
DB:             3        Gaps:       0
US-10-757-745-2 COPY_145_153 (1-9) x BM554324 (1-1035)
QY             1 ProaapVallllepheLaugGIngluVal 9
Dn             605 CCAGATGTGATTAATTCACAGGAAGT 631
RESULT 151      BM926092      1046 bp      mRNA      linear      EST 12-MAR-2002
LOCUS          BM926092
DEFINITION     AGENCOCOURT_6649780 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5764440
VERSION        BM926092.1
KEYWORDS       5', mRNA sequence.
ACCESSION      BM926092.1
SOURCE         GI:19376471
ORGANISM       Homo sapiens (human)
MIMAT          EST.
MIMAT          Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MIMAT          Mammalia; Euteleostomi; Euteleostomi; Primates; Carnivora;
MIMAT          Homnidae; Homo.
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/
AUTHORS        National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE          Unpublished (1999)
JOURNAL        Contact: Robert Strausberg, Ph.D.
COMMENT        Email: cga@bbs-remail.nih.gov
               Tissue Procurement: Life Technologies, Inc.
               cDNA Library Preparation: Life Technologies, Inc.
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.V.G.E. Consortium/LNL at:
               http://image.llnl.gov
               Plate: LHAM12760 row: k column: 11
               High quality sequence stop: 738.
               Location/Qualifiers
                   1..1035
                       /organism="Homo sapiens"
                       /mol_type="mRNA"
                       /db_xref="taxon:9606"
                       /clone="IMAGE:5742466"
                       /tissue_type="medulla"
                       /lab_host="DH10B"
                       /clone_id="NIH_MGC_119"
                       /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
                       Site 2: EcoRV (destroyed); RNA source: normal medulla from
                       anonymous male age 27. Library is oligo-dT primed and
                       directionally cloned (BCRV site is destroyed upon
                       cloning). Average insert size 1.3 kb, insert size range
                       0.9-3 kb. Library is normalized and enriched for
                       full-length clones and was constructed by C. Gher
                       (Invitrogen). Research Genetics tracking code 013. Note:
                       this is a NIH_MGC Library."

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1046)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LHAM12817 row: 0 column: 01
High quality sequence start: 4
High quality sequence stop: 632.
Location/Qualifiers

1..1046
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5764440"
/lab_host="DH10B"
/clone_1b="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV.SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 Kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

ALIGNMENT SCORES:
Pred. No.: 53.9 Length: 1046
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DBs: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BM926092 (1-1046)

OR
1 ProaapValliepheleunglnc1uval 9
|||
DB 306 CCGAGTGTGATATTCTACACGGAAGTT 332

RESULT 152

LOCUS BX337905 1067 bp mRNA linear EST 07-APR-2004
DEFINITION BX337905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1052YNI3 5-PRIME, mRNA sequence.
ACCESSION BX337905
KEYWORDS BX337905.2 GI:46273926
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1067)
L.I.W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30339657.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1046)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LHAM12817 row: 0 column: 01
High quality sequence start: 4
High quality sequence stop: 632.
Location/Qualifiers

1..1046
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5764440"
/lab_host="DH10B"
/clone_1b="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV.SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 Kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

ALIGNMENT SCORES:
Pred. No.: 53.9 Length: 1046
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DBs: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BM926092 (1-1046)

OR
1 ProaapValIIlePheLengIncluvAl 9

DB 306 CCGAGTGTGATATTCTACACGGAAGTT 332

RESULT 152

LOCUS BX337905 1067 bp mRNA linear EST 07-APR-2004
DEFINITION BX337905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1052YNI3 5-PRIME, mRNA sequence.
ACCESSION BX337905
KEYWORDS BX337905.2 GI:46273926
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1067)
L.I.W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30339657.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by life technologies, a
 division of invitrogen. This sequence belongs to sequence cluster
 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cda?ts=CSODI052CG070P1ec=3474.r.
 Location/Qualifiers

FEATURES

source

1..1067
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI052YN13"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	55.1	Length:	1067
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX337905 (1-1067)

Qy 1 Proaapvalli11epheleungl1uval 9
 DB 457 CCAGATGATATTTCTACAGGAGTT 483

RESULT 153

BX444691

LOCUS BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 DEFINITION CSODN005YN02 5-PRIME, mRNA sequence.

ACCESSION BX444691
 VERSION BX444691.2 GI:47009162

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 1081)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

AUTHORS Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)

COMMENT On May 15, 2003 this sequence version replaced gi:30780264.

CONTACT: Genoscope
 Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr; Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by life technologies, a
 division of invitrogen.

This sequence belongs to sequence cluster 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cda?ts=CSODN05D010P1ec=3474.r.

FEATURES

source

1..1081
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODN005YN02"

/issue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_1ib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoR V sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.:	55.9	Length:	1081
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX444691 (1-1081)

Qy 1 Proaapvalli11epheleungl1uval 9

DB 459 CCAGATGATATTTCTACAGGAGTT 485

RESULT 154

CN642527

LOCUS CN642527 1087 bp mRNA linear EST 12-MAY-2004
 DEFINITION ILLUMIGEN MCQ 6530 Katze MPMPL2 Macaca mulatta cDNA clone IBIUM:4699
 5' similar to Bases 1 to 1084 highly similar to human TTRAP
 (Hs.210628), mRNA sequence.

ACCESSION

CN642527.1 GI:47153537
 VERSION CN642527.1

KEYWORDS

SOURCE

ORGANISM

Macaca mulatta (rhesus monkey)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 1087)
 Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
 Proff, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
 Iadonato, S.P.

ANALYSIS of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)

JOURNAL

PUBMED

COMMENT

Contact: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2003.12.24, 840 Q20 bases.
 PCR Primers
 FORWARD: CCTCACCTAAAGGAAACAA
 BACKWARD: CACTATAGGCGGAATTCGCTA
 Insert Length: 1087 Sd Error: 0.00
 Plate: C1000066 row: D column: 10
 Seq primer: CCTCACCTAAAGGAAACAA
 POLYA=No.

FEATURES

source

Location/Qualifiers
 1..1087
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBIUM:4699"
 /sex="male"
 /dev_stage="newborn infant"
 /lab_host="E. coli SOLR"
 /clone_1ib="Katze MPMPL2"
 /note="Organ: Placenta; Vector: Uni-ZAP XR; Site 1: EcoR
 I; Site 2: Xho I; Created from StrataGene ZAP-cDNA

ORIGIN
Synthesis kit (catalog #200400) and ZAP-CDNA GigaPack III
Gold Cloning Kit (Catalog #200450)"

ALIGNMENT SCORES:

Pred. No.:	56.3	Length:	1087
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CN642527 (1-1087)

OY 1 Proapevalli11epheleunglgluval 9

DB 152 CCGAGTGTGATATTTCTACAGAGATT 178

RESULT 155

LOCUS DQ049205 1089 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens TTRAP gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ049205.1 GI:66902404
VERSION DQ049205.1
KEYWORDS SS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
TITLE A scan for positively selected genes in the genomes of humans and
chimpanzees
JOURNAL PLoS Biol. 3 (6), E170 (2005)
PUBMED 1569325

REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05 MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES

source
1..1089
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
<1..>1089
/gene="TTRAP"
/locus_tag="HCL17203"

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	56.4	Length:	1089
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x DQ049205 (1-1089)

OY 1 Proapevalli11epheleunglgluval 9
DB 433 CCGAGTGTGATATTTCTACAGAGATT 459

RESULT 156
DQ049206 1089 bp DNA linear GSS 02-JUN-2005
LOCUS DQ049206
DEFINITION Pan troglodytes TTRAP gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ049206
VERSION DQ049206.1 GI:66902405
KEYWORDS SS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes

REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
TITLE A scan for positively selected genes in the genomes of humans and
chimpanzees
JOURNAL PLoS Biol. 3 (6), E170 (2005)
PUBMED 1569325

REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES
source
1..1089
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1089
/gene="TTRAP"
/locus_tag="HCL17203"

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	56.4	Length:	1089
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x DQ049206 (1-1089)

OY 1 Proapevalli11epheleunglgluval 9

DB 433 CCGAGTGTGATATTTCTACAGAGATT 459

RESULT 157
CN641671 1090 bp mRNA linear EST 12-MAY-2004
LOCUS CN641671
DEFINITION HUMAN MCO 5159 Katze WMR Macaca mulatta cDNA clone IB10W:5970
5' flanked by bases 11 to 990 highly similar to human TTRAP
(HE210628), mRNA sequence.
ACCESSION CN641671.1 GI:47152681
VERSION CN641671.1
KEYWORDS EST
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.
Nielsen,R., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
TITLE A scan for positively selected genes in the genomes of humans and
chimpanzees
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

TITLE Iadonato, S.P.
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 15998449
COMMENT Contact: C. Magness
illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.12.04. 732 Q20 bases.
PCR primers
FORWARD: CCTCCTAAGGAGGACAAAA
BACKWARD: CACTATAGGCGCAATGGGTA
Insert length: 1090 Std Error: 0.00
Plate: CL000043 row: E column: 07
Seq primer: CCTCCTAAGGAGGACAAAA
POLYA=No.

FEATURES

source

1. 1090
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIWM:5970"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze MMRB"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from StrataGene ZAP-cDNA synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
56.4	45.00	100.0%	100.0%	7	
	Matches: 9				
	Conservative: 0				
	Mismatches: 0				
	Indels: 0				
	Gaps: 0				

US-10-757-745-2_COPY_145_153 (1-9) x CN641671 (1-1090)

Qy 1 Proaepvalillepheleugingluval 9
DB 305 CCAGATGATATTTCTACAGAGATT 331

RESULT 158

BM555041 1103 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6545705 NIH_MGC_88 Homo sapiens cDNA IMAGE:5737150
DEFINITION 5', mRNA sequence.
ACCESSION BM555041
VERSION BM555041.1 GI:18795166
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1103)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
Plate: LLM12746 row: m column: 23
High quality sequence atop: 678.

FEATURES

source

1. 1103
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5737150"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH-MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
57.2	45.00	100.0%	100.0%	3	
	Matches: 9				
	Conservative: 0				
	Mismatches: 0				
	Indels: 0				
	Gaps: 0				

US-10-757-745-2_COPY_145_153 (1-9) x BM555041 (1-1103)

Qy 1 Proaepvalillepheleugingluval 9
DB 462 CCAGATGATATTTCTACAGAGATT 488

RESULT 159

CR601303 1168 bp mRNA linear HTC 21-JUL-2004
LOCUS Full-length cDNA clone CSODN005YN02 of Adult Brain of Homo sapiens
DEFINITION (human).
ACCESSION CR601303
VERSION CR601303.1 GI:50482110
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1168)
REFERENCE Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
AUTHORS Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Feng Liang Email: fliang@lifeatech.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Parade Avenue
2 (bases 1 to 1168)
REFERENCE Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: secref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

source

1. 1168
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN005YN02"
/tissue_type="Adult brain"

ORIGIN /plasmid="pCMVSPORT_6"

Alignment Scores:

Pred. No.: 61.1 Length: 1168
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR601303 (1-1168)

OY 1 ProApVal11lephelengingluval 9

DB 458 CCAGATGTGATATTTCTACAGAAAGTT 484

RESULT 160

BM553049 1192 bp mRNA linear EST 20-FEB-2002

LOCUS AGENCOURT_6542413 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5742798

DEFINITION 5', mRNA sequence.

ACCESSION BM553049

VERSION BM553049.1 GI:18791437

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE Homidae; Homo.

JOURNAL 1 (bases 1 to 1192)

COMMENT NIH-MGC http://mgi.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Streusberg, Ph.D.

Email: cga@phs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: L1AM12761 row: 1 column: 07

High quality sequence stop: 747.

Location/Qualifiers

1..1192

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5742798"

US-10-757-745-2_COPY_145_153 (1-9) x BM553049 (1-1192)

OY 1 ProApVal11lephelengingluval 9

DB 490 CCAGATGTGATATTTCTACAGAAAGTT 516

RESULT 161

CR592636 1620 bp mRNA linear HTC 21-JUL-2004

LOCUS full-length cDNA clone CS0DM007YEL1 of fetal liver of Homo sapiens

DEFINITION (human).

ACCESSION CR592636

VERSION CR592636.1 GI:50473443

KEYWORDS HTC; CNSLT_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE Homidae; Homo.

JOURNAL 1 (bases 1 to 1620)

COMMENT Li, W.B., Gruber, C., Jessee, J. and Polyes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue

2 (bases 1 to 1620)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seq@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with NotI and cloned

into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

1..1620

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DM007YEL1"

/tissue_type="Fetal liver"

US-10-757-745-2_COPY_145_153 (1-9) x CR592636 (1-1620)

OY 1 ProApVal11lephelengingluval 9

DB 376 CCAGATGTGATATTTCTACAGAAAGTT 402

RESULT 162

CR602029 1743 bp mRNA linear HTC 21-JUL-2004

LOCUS full-length cDNA clone CS0D1042Y19 of Placenta Cot 25-normalized

DEFINITION of Homo sapiens (human).

ACCESSION CR602029

VERSION CR602029.1 GI:50482836

KEYWORDS HTC; CNSLT_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE Homidae; Homo.

JOURNAL 1 (bases 1 to 1743)

COMMENT

Alignment Scores:

Pred. No.: 88.6 Length: 1620

Score: 45.00 Matches: 3

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 4 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR592636 (1-1620)

OY 1 ProApVal11lephelengingluval 9

DB 376 CCAGATGTGATATTTCTACAGAAAGTT 402

RESULT 162

CR602029 1743 bp mRNA linear HTC 21-JUL-2004

LOCUS full-length cDNA clone CS0D1042Y19 of Placenta Cot 25-normalized

DEFINITION of Homo sapiens (human).

ACCESSION CR602029

VERSION CR602029.1 GI:50482836

KEYWORDS HTC; CNSLT_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE Homidae; Homo.

JOURNAL 1 (bases 1 to 1743)

REFERENCE 1 Homidae; Homo.
AUTHORS 1 (bases 1 to 1743)
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1743)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
1.1743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1042Y1.9"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 96.3 Length: 1743
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x CR602029 (1-1743)

QY 1 Proapvalillepheleungingluval 9
DB 302 CCAGATGATATTTCTACAGAGATT 328

RESULT 163
CR597293 1894 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODK007YK05 of Hela cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR597293
VERSION CR597293.1 GI:50478100
KEYWORDS HTC; CNSLT_CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1894)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1894)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

FEATURES division of Invitrogen.
source
1.1894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK007YK05"
/tissue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 106 Length: 1894
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x CR597293 (1-1894)

QY 1 Proapvalillepheleungingluval 9
DB 451 CCAGATGATATTTCTACAGAGATT 477

RESULT 164
CR595644 1909 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSOD1052Y1N3 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR595644
VERSION CR595644.1 GI:50476451
KEYWORDS HTC; CNSLT_CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1909)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1909)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
1.1909
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1052Y1N3"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 107 Length: 1909
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CG855644 (1-1909)

OY 1 PROASPVALIlePheLeuGlnGluVal 9
DB 457 CCAGATGATGATTTCTCCAGAGATT 483

RESULT 165

CG887267 154 bp mRNA linear GSS 16-JUN-2004
LOCUS CG887267 BayGenomics Gene Trap Library pGTO14f Mus musculus cDNA,
DEFINITION
FEATURES

ACCESSION CG887267.1 GI:38641677

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

FEATURES

source

location/Qualifiers

1..154

/organism="Mus musculus"

/mol_type="cDNA"

/strain="129 o/a"

/db_xref="taxon:10090"

/db_xref="taxon:10090"

/note="Male"

/cell_type="Embryonic stem cell"

/clone_lib="BayGenomics Gene Trap Library pGTO14f"

/note="Vector: pGTO14f"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-757-745-2_COPY_145_153 (1-9) x CG887267 (1-154)

OY

DB

RESULT 166

AZ146818/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

FEATURES

source

location/Qualifiers

1..303

/organism="Strongylocentrotus purpuratus"

/mol_type="genomic DNA"

/db_xref="taxon:7668"

/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"

/note="Organ: Sperm, Vector: BAC3.6, BAC Clones in E-Coli DH10B"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-757-745-2_COPY_145_153 (1-9) x AZ146818 (1-303)

OY

DB

RESULT 167

BCG91909

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

FEATURES

source

location/Qualifiers

1..410

/organism="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"

/note="Organ: Sperm, Vector: BAC3.6, BAC Clones in E-Coli DH10B"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-757-745-2_COPY_145_153 (1-9) x BCG91909 (1-410)

OY

DB

RESULT 168

AZ146818/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

FEATURES

source

location/Qualifiers

1..410

/organism="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"

/note="Organ: Sperm, Vector: BAC3.6, BAC Clones in E-Coli DH10B"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-757-745-2_COPY_145_153 (1-9) x AZ146818 (1-303)

OY

DB

Page 78

phosphate-free) "

436
Monthly

```

36.2 2/3  

44.00  

100.0%  

88.9%  

97.8%  

7  

  lensin: 8  

  matches: 8  

  conservative: 1  

  mismatches: 0  

  indels: 0  

  gaps: 0

```

5_153 (1-9) x CK993559 (1-476)

IIepheLeuGIInIuVal 9
|||||
ATCTTCCTCCAAGAGTC 274

	484 bp	mRNA	linear	EST 28-NOV-2002
CSEGCN66	Gallus gallus	CDNA clone	ChEST314c1	5', mRNA

GI:25846912
us (chicken)
us

Metazoa; Chordata; Craniata; Euteleostomi;
; Aves; Neognathae; Galliformes; Phasianidae;
; Gallus.
(to 484)

12 (22), 1965-1969 (2002
mon Hubbard

Manchester, M60 1QD, UK
108930
60409
on.hubbard@umist.ac.uk.

Education/Qualifiers
.484

`%organism="Gallus gallus"
%ol_type="mRNA"
%strain="White Leghorn, Hisex"
%taxon="9031"
%chr="CHS714c1"
%stage="16 day embryo"
%host="DH10B"
%clone_id="CS8CCHN66"
%notrailer="Organ: brain; Vector: pBlueScript II KS(+); Site: 1
%site2=NotI; This normalized library was
constructed from 1 million independent clones. cDNA
libraries were initiated using an oligo(dT) primer, using
the following C in the first strand synthesis reaction.
This first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
NotI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBlueScript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
91: 9228-9232 and Bonardo et al., Genome Research
5: 791, except that a significantly longer
annealing hybridization was used."`

36.9	Length:	484
44.00	Matches:	8

```
Conservative: 1
Mismatches: 0
Indels: 0
Gaps: 0
```

U338911 (1-484
val 9
|||
STT 110

93 bp mRNA linear EST 16-FEB-1997
DMS Mus musculus cDNA clone IMAGE:598816

0
1
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5
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A
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K
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N
O
P
Q
R
S
T
U
V
W
X
Y
Z

ridae; Muriinae; Mus:

Project
Project

College of Medicine
Box 8501, St. Louis, MO 63108
t.edu
valley-free through LNL ; contact the
ge.llnl.gov) for further information.
om Amersham
: 480.

82

"accus"
 "0090"
 "816"
 "ean"
 "ke"
 "mouse 3NBMS"
 "73D-Pac (Pharmacia) with a modified
 "1: Not I; Site2: Eco RI; 1st strand cDN
 "Not I - oligo(dT) primer 15"
 "GCGGCGCGCGCTGTGTGTGTGTGTGTGTGT
 "used cDNA was ligated to Eco RI adaptore
 "labeled with Not I and cloned into the Not
 "of the modified pT73 vector. RNA
 "transcribed with Not I and digested through
 "restriction Jordan. Library went through
 "normalization, and was constructed by
 "M.Felima Bonaldo."

```
Matches:      8
Conservative: 1
Mismatch:     0
```

Query Match: 97.8% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AA163045 (1-493)

Qy 1 ProapvalillepHeuengIngluval 9
DB 140 CCAGATGTGTATTCTACAGGAAGTT 166

RESULT 172

CC248786 517 bp mRNA linear GSS 13-MAY-2003
LOCUS CC248786
DEFINITION XK529 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA, mRNA sequence.

ACCESSION CC248786
VERSION CC248786.1 GI:30585518
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Sciurognathi; Muroidea; Euarctontoglires; Glires; Rodentia;
JOURNAL 1 (bases 1 to 517)
COMMENT BayGenomics.
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from http://baygenomics.ucsf.edu/cgi-bin/Baysearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=XK529

FEATURES
source location/Qualifiers
1..517
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/note="Vector: pGT0Lxf"

ORIGIN

Alignment Scores:

Pred. No.:	39.8	Length:	517
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	9	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CC248786 (1-517)

Qy 1 ProapvalillepHeuengIngluval 9
DB 143 CCAGATGTGTATTCTACAGGAAGTT 169

RESULT 173

BE290901 525 bp mRNA linear EST 13-JUL-2000
LOCUS BE290901
DEFINITION 601084205F1 NCI_CGAP_Mame Mus musculus cDNA clone IMAGE:3498336 5', mRNA sequence.

ACCESSION BE290901
VERSION BE290901.1 GI:9172261
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE
AUTHORS Sciurognathi; Muroidea; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8553 row: j column: 01
High quality sequence stop: 500.
Location/Qualifiers
1..525
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3498336"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mame"
/note="Organ: mammary; Vector: PCWV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Alignment Scores:

Pred. No.:	40.5	Length:	525
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BE290901 (1-525)

Qy 1 ProapvalillepHeuengIngluval 9
DB 171 CCAGATGTGTATTCTACAGGAAGTT 197

RESULT 174

CN233559 531 bp mRNA linear EST 09-APR-2004
LOCUS RJA113F02.ab1 Rubrain Gallus gallus cDNA 5', mRNA sequence.
DEFINITION CN233559
ACCESSION CN233559
VERSION CN233559.1 GI:4637303
KEYWORDS EST.

SOURCE Gallus gallus (chicken)
ORGANISM

REFERENCE
AUTHORS Savolainen, P., Flitzsimmons, C.J., Arvestad, L., Andersson, L. and Lundberg, J.
EST analysis of brain and testis cDNA libraries from white leghorn and Red Jungle Fowl
Unpublished (2004)
Contact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0) 8 5537 8481
Fax: +46 (0) 8 5537 8335
Email: Peter.Savolainen@biotech.kth.se

JOURNAL COMMENT

Seq primer: M13 reverse primer.
Location/Qualifiers

1. 531
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Red junglefowl"
/db_xref="taxon:9031"
/sex="female"
/lab_host="ElectronMAX DH10B (Invitrogen)"
/clone_lib="RDBrain"
/note="Organ: brain; Vector: pSPORT-1; Site_1: Hind III;
Site_2: EcoRI; The cDNA libraries were created with the
Superscript plasmid system (Invitrogen)."

ORIGIN

Alignment Scores:

Pred. No.:	41	Length:	531
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CN233559 (1-531)

QY 1 Proaspva111epheleunglunva1 9

DB 393 CCAGATGCTGCTTTTACAGAGCTT 419

RESULT 175

CD321260

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD321260 541 bp mRNA linear EST 17-SEP-2003
Strp538.002622 Sea urchin embryo 7hr cleavage stage cDNA library
MEMG538 Strongylocentrotus purpuratus cDNA clone
CALTP58D0924;MPL_538_24D9 5', mRNA sequence.
CD321260.1 GI:34793321
EST.
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinoidea; Echinacea; Echinoidae;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 541)
Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A.,
Reinhardt, R., Herwig, R., Panopoulou, G., and Jehrach, H.
Generation, annotation, evolutionary analysis, and database
integration of 20,000 unique sea urchin EST clusters
Genome Res. 13 (12), 2736-2746 (2003)
Contact: Poustka AJ
Laboratory 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Insestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: Poustka@molgen.mpg.de
The library was characterized by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/eg_seaurchin/. cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (<http://www.rzpd.de>)
PCR Primers
FORWARD: 5' CCCAGGCTTACATTATGCTCCGGCTG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTAGCGAGCTCGGAAAGGAGATGG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGCTCGGAAATCCCGGT-3' pSPORT3/86
High quality sequence stop: 541.

FEATURES

source

Location/Qualifiers
1. 541
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="CALTP58D0924;MPL_538_24D9"
/tissue_type="whole embryo"
/dev_stage="embryonic 7hr"
/lab_host="E.coli, Xui blue"
/clone_lib="Sea urchin embryo 7hr cleavage stage cDNA
library MEMG538"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Random
primed and directionally cloned in pSPORT1 using a
NotI (5'-pACTAGTTCTAGATCGGAGCGGCGCCGCTT)153' and a
SalI 5'-TCATCCACGATCG-3' adapters (Gibco BRL)."

ORIGIN

Alignment Scores:

Pred. No.:	41.9	Length:	541
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CD321260 (1-541)

QY 1 Proaspva111epheleunglunva1 9

DB 288 CCAGATGCTGCTTTTCCAGAGCTG 314

RESULT 176

AA208842

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA208842 544 bp mRNA linear EST 18-FEB-1997
mw73d02.71 Soares mouse NML Mus musculus cDNA clone IMAGE:676323
5', mRNA sequence.
AA208842.1 GI:1806779
EST.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 544)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steppe, M., Tan, F., Underwood, K., Moore, B.,
Thaising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The Mashu-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.lln.gov) for further information.
MGI:416027
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 491.
Location/Qualifiers
1. 544
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:676323"
/tissue_type="Liver"
/lab_host="DH10B"
/clone_lib="Soares mouse NML"

ORIGIN

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCCGCGAATGCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 42.2	544	8	1	0	0	0
Percent Similarity: 44.00						
Best Local Similarity: 100.0%						
Query Match: 97.8%						

US-10-757-745-2_COPY_145_153 (1-9) x AA208842 (1-544)

Qy 1 ProaepValIlePheLeuGlnGluVal 9

Db 269 CCAGATGTGTATTTCTACAGAGATT 295

RESULT 177

LOCUS AA476073 547 bp mRNA linear EST 18-JUN-1997
DEFINITION vnt26906.r1 Soares mammary_gland_NBMNG Mus musculus CDNA clone
IMAGE:876634 5', mRNA sequence.

ACCESSION AA476073
VERSION AA476073.1 GI:2203924

KEYWORDS EST

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubugue, T.,
Getzel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterson, R.

The WashU-HMI Mouse EST Project
Unpublished (1996)

JOURNAL

Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:516114
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 493.

Location/Qualifiers
1..547

FEATURES

source

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:876634"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_11b="Soares_mammary_gland_NBMNG"
/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand CDNA was primed with a Not I -

ORIGIN

oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCCGCGAATGCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded CDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 42.4	547	8	1	0	0	0
Percent Similarity: 44.00						
Best Local Similarity: 100.0%						
Query Match: 97.8%						

US-10-757-745-2_COPY_145_153 (1-9) x AA476073 (1-547)

Qy 1 ProaepValIlePheLeuGlnGluVal 9

Db 501 CCAGATGTGTATTTCTACAGAGATT 527

RESULT 178

LOCUS BG148976 552 bp mRNA linear EST 01-FEB-2001
DEFINITION u87b07.y1 Soares mouse_NMGB bcell Mus musculus CDNA clone
IMAGE:338338 5', similar to FR:095551 095551 D330M3.3, mRNA
sequence.

ACCESSION BG148976
VERSION BG148976.1 GI:12652398

KEYWORDS EST

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL

Other ESTs: u87b07.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1088384
Seq primer: -40RP from Gibco
High quality sequence stop: 455.

Location/Qualifiers
1..552

FEATURES

source

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:338338"
/lab_host="DH10B (phage-resistant)"
/clone_11b="Soares mouse_NMGB bcell"
/note="Organ: germinal B-cell; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand CDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCCGCGAATGCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded CDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized; constructed by Bento Soares and
M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	Length:
42.9	552

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Pred. No.: 43.4

DB: 5

QY 1 ProaspVal1lePheLeuGlnGluVal 9
 |||||.....
 DB 170 CCAGATGTGCTGTTTACAGAGAGTT 196

RESULT 181
 LOCUS B1444674
 DEFINITION de27d10.y3 Wellcome CRC PRN3 oocyte Xenopus laevis cDNA clone
 IMAGE:3472962.5, similar to TR:095551.095551.DJ30M3.3, mRNA
 sequence.

ACCESSION B1444674
 VERSION B1444674.1 GI:15269381
 KEYWORDS EST
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 581)
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L.,
 Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.,
 Person, B., Gibbons, M., Harvey, N., Rittner, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 WashU Xenopus EST project, 1999
 Unpublished (1999)
 CONTACT: Sandy Clifton, Ph.D.
 WashU Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.
 Gurdon (Wellcome/CRC Institute). DNA sequencing by: Washington
 University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/HLN at: info@image.lln.gov
 High quality sequence stop: 403.

FEATURES
 Location/Qualifiers
 1..581
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:3472962"
 /tissue_type="oocyte"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Wellcome CRC PRN3 oocyte"
 /note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
 were oligo-dT primed and directionally cloned. Sequencing
 according to Nieuwkoop and Faber. Library was constructed
 by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon
 (Wellcome/CRC Institute)."

ORIGIN

Alignment Scores:
 Pred. No.: 45.4 Length: 581
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1444674 (1-581)

QY 1 ProaspVal1lePheLeuGlnGluVal 9
 |||||.....
 DB 333 CCAGATGTGCTGTTTACAGAGAGTT 359

RESULT 182
 LOCUS B1064472
 DEFINITION pgfin.pk001.h17,normalized chicken fat cDNA library Gallus gallus

CDNA clone pgfin.pk001.h17.5, similar to gi|7705262
 ref|NP_057698.1| TRAF and TNF receptor-associated protein [Homo
 sapiens] gb|AA64144.1|AF223469_1 (AF223469) AD022 protein [Homo
 sapiens]g, mRNA sequence.

ACCESSION B1064472
 VERSION B1064472.1 GI:14471994
 KEYWORDS EST
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 600)
 Cogburn, L.A., Morgan, R.W. and Burnside, J.
 Chicken ESTs from fat
 Unpublished (2001)
 CONTACT: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
 Location/Qualifiers
 1..600
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="pgfin.pk001.h17"
 /sex="Male and Female"
 /tissue_type="fat"
 /lab_host="E.coli BMD10B"
 /clone_lib="normalized chicken fat cDNA library"
 /note="Vector: pSPORT1"

ORIGIN

Alignment Scores:
 Pred. No.: 47.1 Length: 600
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1064472 (1-600)

QY 1 ProaspVal1lePheLeuGlnGluVal 9
 |||||.....
 DB 329 CCAGATGTGCTGTTTACAGAGAGTT 355

RESULT 183
 LOCUS B1990829
 DEFINITION 4081-88 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
 mRNA sequence.

ACCESSION B1990829
 VERSION B1990829.1 GI:17961846
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 600)
 Mu, X., Zhao, S., Perahad, R., Haieh, T.-F., Scarpa, A., Wang, S.W.,
 White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
 Gene expression in the developing mouse retina by EST sequencing
 and microarray analysis
 Nucleic Acids Res. 29 (24), 4983-4993 (2001)

JOURNAL PUBLISHED 11812828
 CONTACT: Klein WH
 Department of Biochemistry and Molecular Biology
 University of Texas M.D. Anderson Cancer Center
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA

Thu Mar 16 10:39:26 2006

US-10-757-745-2_copy_145_153.rst

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Tel: 713 792 3646
Fax: 713 790 0329
Location/Qualifiers
1..600
source

FEATURES
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_1fb="Mouse E14.5 retina lambda ZAP II library"

ORIGIN

Alignment Scores:
Pred. No.: 47.1 Length: 600
Score: 44.00 Matches: 9
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1990829 (1-600)

OY 1 PROAPVAL11EPHELENGINGUVA1 9
DB 496 CCAGATGTGTATTTCTACAGAGATT 522

RESULT 184
CBS79756 615 bp mRNA linear EST 03-APR-2003
LOCUS AMGNOC:NRD1-00175-B9-A nrdg1 (10855) Rattus norvegicus cDNA clone
DEFINITION nrdg1-00175-e9 5', mRNA sequence.
ACCESSION CBS79756
VERSION CBS79756.1 GI:29523797
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Bukarya; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 615)

REFERENCE
AUTHORS Amgen Rat EST Program
TITLE Unpublished (2003)
JOURNAL
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00175 row: e column: 9.

FEATURES
source
1..615
Location/Qualifiers

/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrdg1-00175-e9"
/tissue_type="dorsal root ganglia"
/clone_1fb="nrdg1.0855"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
dorsal root ganglia"

ORIGIN

Alignment Scores:
Pred. No.: 48.5 Length: 615
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CBS79756 (1-615)

OY 1 PROAPVAL11EPHELENGINGUVA1 9
DB 507 CCGACGTGTATTTCTACAGAGATT 533

RESULT 185
CN694288 617 bp mRNA linear EST 18-MAY-2004
LOCUS E0348E09-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus
DEFINITION musculus cDNA clone NIA:E0348E09 IMAGE:30863576 5', mRNA sequence.
ACCESSION CN694288
VERSION CN694288.1 GI:47463037
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 617)
REFERENCE
AUTHORS Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,
VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Baese, U.C.,
Wang, Y., Carter, M.G., Hamatani, T., Alpa, K., Akutsu, H., Sharov, L.,
Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,
Nageraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,
Schlesinger, D., Keller, J., Klotz, E., Klesse, G., Umezawa, A.,
Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,
D'Urso, M., Klesse, J., Hide, W., and Ko, M.S.
TITLE Transcriptional analysis of mouse stem cells and early embryos
JOURNAL Plos Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: E0348 row: E column: 09
Seq primer: M13 Reverse
High quality sequence stop: 617
POLYA=No.
FEATURES
source
1..617
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="NIA:E0348E09 IMAGE:30863576"
/tissue_type="whole embryo including extraembryonic
tissues at 10.5-days postcoitum"
/dev_stage="E10.5"
/lab_host="DH10B"
/clone_1fb="NIA Mouse E10.5 whole embryo cDNA library
(Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
Site_2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library. Total
Genome Res. 11: 1553-1558 (2001). [PMID: 11544197] 5-days
RNAs were extracted from a pool of 8 embryos at 10.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen:
5'-pGACTGTTCTGATCGGAGCGCCGCCCTTTTCTTTT-3'] from
2ug of total RNA, treated with 74 DNA polymerase, and
ligated to linker L1-SalI, purified by phenol/chloroform and
separated from free linker by centrifugation. The cDNAs were ligated
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The using
products were purified by phenol/chloroform and centrifuged
100. The cDNAs were digested with SalI and NotI enzymes
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 3.4kb. The library was
constructed by Yulan Piao."

Alignment Scores:

Pred. No.: 48.7 Length: 617
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CNG94288 (1-617)

Qy 1 ProaspVal1lePheLeuGlnGluVal 9
 Db 92 CCAGATGCTGTATTCTTACAGAGAGTT 118

RESULT 186

BF182465 621 bp mRNA linear EST 31-OCT-2000
 LOCUS 601804232F1 NCI_CGAP_Mams Mus musculus cDNA clone IMAGE:4035319 5',
 DEFINITION mRNA sequence.
 ACCESSION BF182465.1 GI:11060608
 VERSION BF182465.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strassberg, Ph.D.
 COMMENT Email: cga@db-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9308 row: P column: 08
 High quality sequence stop: 615.
 Location/Qualifiers

FEATURES

1..621
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="mix FVB/N, C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:4035319"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /clone_1lb="NCI CGAP Mams"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

ORIGIN

Alignment Scores:

Pred. No.: 49 Length: 621
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF182465 (1-621)

Qy 1 ProaspVal1lePheLeuGlnGluVal 9
 Db 495 CCAGATGCTGTATTCTTACAGAGAGTT 521

RESULT 187

BU471395 625 bp mRNA linear EST 30-NOV-2002
 LOCUS 603163114F1 CSEQRBN21 Gallus gallus cDNA clone CHEST258K3 5', mRNA
 DEFINITION sequence.
 ACCESSION BU471395.1 GI:25964972
 VERSION BU471395.1
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE Boardman, P.E., Sanz-Ezquerro, V., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

1..625
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer"
 /db_xref="taxon:9031"
 /clone="CHEST258K3"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="CSEQRBN21"
 /note="Organ: ovary; Vector: pBluescript II KS(+); Site 1:
 EcoRI; Site 2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.: 49.4 Length: 625
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BU471395 (1-625)

Qy 1 ProaspVal1lePheLeuGlnGluVal 9
 Db 376 CCAGATGCTGTATTCTTACAGAGAGTT 402

RESULT 188

CD807796 625 bp mRNA linear EST 15-JUL-2003
 LOCUS CD807796
 DEFINITION UI-M-GWO-clq-g-15-0-UI.r1 NIH_BMAP_GWO Mus musculus cDNA clone

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 86

IMAGE:30539966 5', mRNA sequence.
ACCESSION CB807786
VERSION CD807796.1 GI:32466622
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS NIH (bases 1 to 625)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gstraus@remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this CDNA
sequence: 215-278, >IDS#SINE/ID (matched complement)
Seq primer: PIX-5.

FEATURES
source
1..625
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="TMAGS:30539966"
/tissue_type="whole eye"
/dev_stage="embryo.15.5,16.5,17.5,18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP-GM0"
/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoRI I;
Site 2: Not I; The library was constructed according
to Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoRI adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CCGCGTCTCC. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	49.4	Length:	625
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CD807796 (1-625)

QY 1 Proaapvalli1lephelenglnqluval 9

Db 459 CCGAGATGTGTATTCTACAGAGAGTT 485

RESULT 189 CB577890 627 bp mRNA linear EST 03-APR-2003
LOCUS CB577890
DEFINITION AMGNNUC:NRDQ1-00195-C6-A nrdq1 (10855) Rattus norvegicus CDNA clone
nrdq1-00195-c6 5', mRNA sequence.

ACCESSION CB577890
VERSION CB577890.1 GI:29521931
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
REFERENCE Angen Rat EST Program
AUTHORS Angen Rat EST Program
TITLE Unpublished (2003)
JOURNAL Contact: Dan Fitzpatrick
COMMENT Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805.447.4881
Plate: 00195 row: C Column: 6.

FEATURES
source
1..627
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrdq1-00195-c6"
/tissue_type="dorsal Root Ganglia"
/clone_id="nrdq1 (10855)"
/note="Vector: pSPOR1, Site 1: SalI, Site 2: NotI, rat
dorsal root ganglia"

ORIGIN

Alignment Scores:

Pred. No.:	49.6	Length:	627
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CB577890 (1-627)

QY 1 Proaapvalli1lephelenglnqluval 9

Db 537 CCGAGATGTGTATTCTACAGAGAGTT 563

RESULT 190

AL858410 634 bp mRNA linear EST 02-DEC-2003
LOCUS AL858410
DEFINITION AL858410 XGC-egg Xenopus tropicalis CDNA clone TB95059p03 5', mRNA
sequence.

ACCESSION AL858410.2 GI:38633375

VERSION AL858410.2

KEYWORDS EST.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE Xenopus EST Program
AUTHORS Xenopus EST Program
TITLE Unpublished (2003)
JOURNAL On Sep 15, 2002 this sequence version replaced gi:22878591.
COMMENT Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger@ac.uk
Sanger Xenopus EST project 2001
TROPCALUS_SEQUENCE_ID: TB95059p03.PIXS6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
CDNA was oligo dT primed from 5ug of poly A+ RNA from egg
EcoRI-NotI cut CDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers

FEATURES
source 1..634
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TE95059p03"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_1ib="XGC-egg"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dt primed from 5'ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"

ORIGIN

Alignment Scores:

Pred. No.:	50.2	Length:	634
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AB858410 (1-634)

Qy 1 ProaSpVal1lePheLeuGInGluVal 9
|||||:|||||
Db 436 CCAGATGTAGTATTCTTACAGAGGTT 462

RESULT 191

DN091361 634 bp mRNA linear EST 14-FEB-2005
LOCUS JGI CABE4216.fwd NIH XGC tropOval Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7822728 5', mRNA sequence.
DN091361
VERSION DN091361.1 GI:59758465
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 634)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI CABE4216.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Bruce Blumberg Laboratory, University of
California, Irvine
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNL:
http://image.jnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Place: CABR 0041 row: p column: 22
High quality sequence stop: 575.
Location/Qualifiers

FEATURES

source 1..634
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"

ORIGIN

Pred. No.:	50.2	Length:	634
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	8	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x DN091361 (1-634)

Qy 1 ProaSpVal1lePheLeuGInGluVal 9
|||||:|||||
Db 280 CCAGATGTAGTATTCTTACAGAGGTT 306

RESULT 192

BM539358 635 bp mRNA linear EST 20-FEB-2002
LOCUS hb08d09.g1 Canis CDNA from testes cells Canis familiaris cDNA
DEFINITION clone hb08d09 5', mRNA sequence.
BM539358
VERSION BM539358.1 GI:18821216
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 635)
O'Shaughnessy, A.L., McCombie, W.R., Baker, J.P., Balija, V.,
Cumini, D., Dedhia, N.N., de la Bastide, M., Katzenberger, P.,
King, L., Kirchoff, K.A., Miller, B., Miller, S., Nascimento, L.U.,
Palmer, L., Santos, L., Shah, R.S., Spiegel, L.A., Zucavern, T.,
Preston, R. and Hammon, G.J.
Expressed sequence tags from Canis familiaris (dog) (2002)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Place: hb08 row: d column: 09
Seq primer: -21M3UnivRev
High quality sequence stop: 635.
Location/Qualifiers

FEATURES

source 1..635
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"

/clone="hb08d09"
/tissue_type="testes"
/clone_id="Canis CDNAs from testes cells"
/note="Vector: Lambda Zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stragene zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."

ORIGIN

Alignment Scores:

Pred. No.: 50.3 Length: 635
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BMS39358 (1-635)

Qy 1 Proaapvalilepheleuglnqluval 9

Db 249 CCAGATGCTGATATTTCTACAGGAGTC 275

RESULT 193
AL0901140

LOCUS AL0901140 638 bp mRNA linear EST 04-DEC-2003
DEFINITION XGC-egg Xenopus tropicalis cDNA clone TB9077f04 5', mRNA sequence.

ACCESSION AL0901140

VERSION AL0901140.2 GI:38699862

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Sep 16, 2002 this sequence version replaced gi:22953375.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS_SEQUENCE_ID: TB9077f04.plksp6

Sequencing primer: SP6

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.

ECORI-NotI cut cDNA was then ligated into pCS107 with EORI at the

5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EORI; Site 2: NotI

Host: Escherichia coli XL1-blue.

Location/Qualifiers

1..638

/organism="Xenopus tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="TB9077f04"

/dev_stage="egg"

/lab_host="Escherichia coli XL1-blue"

/clone_lib="XGC-egg"

/note="Vector: pCS107; Site 1: EORI; Site 2: NotI; cDNA

was oligo dt primed from 5ug of poly A+ RNA from egg.

ECORI-NotI cut cDNA was then ligated into pCS107 with

ECORI at the 5' end and NotI at the 3' end"

ORIGIN

Alignment Scores:

Pred. No.: 50.5 Length: 638
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AL0901140 (1-638)

Qy 1 Proaapvalilepheleuglnqluval 9

Db 311 CCAGATGCTGATATTTCTACAGGAGTC 337

RESULT 194

CB545297

LOCUS CB545297

DEFINITION AMGNNUC:NR001-00108-F11-A nr001 (10855) Rattus norvegicus cDNA

clone nr001-00108-f11 5', mRNA sequence.

ACCESSION CB545297

VERSION CB545297.1 GI:29429238

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Amgen, Inc

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00108 row: f column: 11.

Location/Qualifiers

1..639

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="nr001-00108-f11"

/tissue_type="Dorsal Root Ganglia"

/clone_lib="nr001 (10855)"

/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat

dorsal root ganglia"

ORIGIN

Alignment Scores:

Pred. No.: 50.6 Length: 639
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CB545297 (1-639)

Qy 1 Proaapvalilepheleuglnqluval 9

Db 416 CCAGATGCTGATATTTCTACAGGAGTC 442

RESULT 195

AL054676

LOCUS AL054676

DEFINITION AL054676 XGC-egg Xenopus tropicalis cDNA clone TB9019p19 5', mRNA

sequence.

ACCESSION AL054676

VERSION AL054676.2 GI:38630173

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Xenopus tropicalis (western clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

REFERENCE
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 640)
AUTHORS
Crouling, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M., and Rogers, J.
TITLE
Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL
Unpublished (2003)
COMMENT
On Sep 15, 2002 this sequence version replaced gi:22874895.
Contact: Taylor R

Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEG9019p19.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NciI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NciI at the 3' end.
Vector: pCS107, Site 1: EcoRI; Site 2: NciI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1..640
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEG9019p19"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NciI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NciI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NciI at the 3' end"

ORIGIN

Alignment Scores:
Pred. No.: 50.7 Length: 640
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x ALB54676 (1-640)

QY 1 Proaepvalilpheleunglgluval 9
DB 456 CCAGATGTAGTATTCTTACAGAGGTT 482

RESULT 196

LOCUS BG083167 644 bp mRNA linear EST 18-DEC-2003
DEFINITION H3085C02-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3085C02 5', mRNA sequence.
ACCESSION BG083167
VERSION BG083167.2 GI:40069892
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euteleostomi; Euteleostomi; Euteleostomi;
Schuognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 644)

REFERENCE

Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.U., Wang, X.,
Gratovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagarsa, R., Doi, H.,
Wood, M.H., III, Becker, K.G., and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse development cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

TITLE

JOURNAL PUMED
On Jan 26, 2001 this sequence version replaced gi:12565735.
Other ESTs: H3085C02-3

COMMENT
Contact: George J. Kargul

FEATURES
source
1..644
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="nabst:H3085C02-5"
/db_xref="taxon:10090"
/clone="H3085C02"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
libraries"
/lab_host="DH10B"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/note="Vector: pSPORNT; Site 1: SalI; Site 2: NciI; This
clone is among a rearranged set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, embryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dt)-Not primers. References include: (1)
genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97:
9127-9132; (2) large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
development, 2000, Development, 127: 1737-1749; (3)
genome-wide mapping of unselected transcripts from
extremembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Alignment Scores:
Pred. No.: 51.1 Length: 644
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG083167 (1-644)

QY 1 Proaepvalilpheleunglgluval 9
DB 229 CCAGATGTAGTATTCTTACAGAGGTT 255

RESULT 197

LOCUS BM426270 645 bp mRNA linear EST 30-JAN-2002
DEFINITION pGf2n.pX002.c6 Normalized Chicken Abdominal Fat Library (pGf2n)
Gallus gallus cDNA clone pGf2n.pX002.c6 5' similar to g111418470
ref[XP_004263.1] TRAF and TNF receptor-associated protein [Homo
sapiens] g114747264 ref[XP_041298.1] TRAF and TNF
receptor-associated protein [Homo sapiens] emb[CAC21141.1]
(AU031755) d330M3.3 (novel protein similar to C. elegans, mRNA
sequence.
ACCESSION BM426270
VERSION BM426270.1 GI:18430455
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_pzn model

Run on: March 16, 2006, 00:29:49 ; Search time 6832.46 Seconds

(without alignments)
595.756 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_140

Perfect score: 448
Sequence: 1 MERALNSYFPPPEVESALER.....IDGLDNLNLSERAGVCYL 87

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Command line parameters:
-MODEL=frame2_pzn.model -DEV=xlh
-O=/abs/ABSSMBE/spool/US10757745/runat_15032006_165652_3610/app_query.fasta_1
-DB=EST -QFMT=fastadp -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.cdi -LIST=1000
-DOCLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=200 -MODE=LOCAL
-OUTFMT=pcg -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02h
-USER=US10757745@CGN_1_1.8148@runat_15032006_165652_3610 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: +
1: gb_esc1: +
2: gb_esc2: +
3: gb_esc3: +
4: gb_hic: +
5: gb_esc4: +
6: gb_esc5: +
7: gb_esc6: +
8: gb_esc7: +
9: gb_ges1: +
10: gb_ges2: +
11: gb_ges3: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	429	5	BO582059 1112611.Y
2	448	100.0	471	5	CR543841 DKFZ04590
3	448	100.0	473	6	CB120224 K-EST0167
4	448	100.0	480	1	A1750554 CN04601.Y
5	448	100.0	485	1	AA486032 ab40b10.Y
6	448	100.0	530	3	BM846221 K-EST0125
7	448	100.0	554	3	BP220985 BP220985

8	448	100.0	565	3	BP226620
9	448	100.0	566	3	BP220508
10	448	100.0	568	3	BP257211
11	448	100.0	570	3	BP221518
12	448	100.0	573	1	AU279894
13	448	100.0	573	3	BP221260
14	448	100.0	573	3	BP261500
15	448	100.0	576	3	BP262642
16	448	100.0	577	7	CN298919
17	448	100.0	580	3	BP274368
18	448	100.0	581	3	BP207751
19	448	100.0	581	3	BP225088
20	448	100.0	581	3	BP262638
21	448	100.0	581	3	BP270744
22	448	100.0	581	3	BP379659
23	448	100.0	582	3	BP219740
24	448	100.0	582	3	BP261141
25	448	100.0	582	3	BP270415
26	448	100.0	582	3	BP275810
27	448	100.0	583	3	BP195721
28	448	100.0	583	3	BP262103
29	448	100.0	583	3	BP262741
30	448	100.0	583	3	BP319548
31	448	100.0	583	5	BU783329
32	448	100.0	584	3	BP263059
33	448	100.0	584	3	BP348623
34	448	100.0	588	3	BP236074
35	448	100.0	602	1	AL703449
36	448	100.0	621	6	CB069952
37	448	100.0	634	6	CB157906
38	448	100.0	634	7	CY023369
39	448	100.0	642	7	BI333830
40	448	100.0	644	7	CR753214
41	448	100.0	657	7	CN298920
42	448	100.0	678	2	CG119113
43	448	100.0	701	5	CR672326
44	448	100.0	710	7	BU661472
45	448	100.0	711	7	CN298923
46	448	100.0	729	7	CN298922
47	448	100.0	729	7	CN298922
48	448	100.0	731	8	CK760857
49	448	100.0	767	2	BI258848
50	448	100.0	774	3	BI754101
51	448	100.0	786	2	BI719977
52	448	100.0	799	8	CG756424
53	448	100.0	810	8	CX166335
54	448	100.0	838	3	BI908925
55	448	100.0	846	7	CR765451
56	448	100.0	853	2	BE784416
57	448	100.0	858	3	BI553412
58	448	100.0	870	2	BG740396
59	448	100.0	870	5	BU159911
60	448	100.0	883	5	BU169945
61	448	100.0	883	5	BU179107
62	448	100.0	906	6	CD251503
63	448	100.0	937	2	BS541819
64	448	100.0	948	1	AL555333
65	448	100.0	959	2	BI161201
66	448	100.0	972	3	BM468826
67	448	100.0	981	5	BX338160
68	448	100.0	995	2	BB892886
69	448	100.0	1018	5	EX337141
70	448	100.0	1035	4	BM554324
71	448	100.0	1067	5	EX337905
72	448	100.0	1081	5	EX444691
73	448	100.0	1089	11	DO049205
74	448	100.0	1103	4	BM555041
75	448	100.0	1168	4	CR601303
76	448	100.0	1192	3	BM553049
77	448	100.0	1620	4	CR592636
78	448	100.0	1894	4	CR597293
79	448	100.0	1909	4	CR595644
80	448	99.3	581	1	AV717253

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81	444	59.1	582	3	BP234218	BP234218	154	211.5	47.2	600	3	BT990829	BT990829
82	443	58.2	582	3	BP233592	BP233592	155	211.5	47.2	645	1	BT737520	BT737520
83	443	58.2	572	3	BP262485	BP262485	156	211.5	47.2	648	1	AM216803	AM216803
84	440	58.2	582	3	BP263516	BP263516	157	211.5	47.2	651	3	BT648868	BT648868
85	440	58.2	582	3	BP977971	BP977971	158	211.5	47.2	767	8	BT226137	BT226137
86	440	58.2	582	3	BP358707	BP358707	159	211.5	47.2	841	2	BT784192	BT784192
87	440	58.2	582	3	BP926092	BP926092	160	211.5	47.2	942	2	BT298330	BT298330
88	440	58.2	582	3	BP926092	BP926092	161	211.5	47.2	963	3	BT156151	BT156151
89	440	58.2	582	3	BP926092	BP926092	162	211.5	47.2	1046	6	BT165386	BT165386
90	440	58.2	582	3	BP926092	BP926092	163	211.5	47.0	615	6	BT579756	BT579756
91	439	58.0	752	1	BP926092	BP926092	164	210.5	47.0	627	6	BT579756	BT579756
92	437	57.5	739	5	BP365835	BP365835	165	210.5	47.0	639	7	BT579756	BT579756
93	436	57.3	780	5	BP365835	BP365835	166	210.5	46.1	734	6	BT579756	BT579756
94	435	57.1	780	5	BP365835	BP365835	167	201	44.9	640	1	BT579756	BT579756
95	435	57.1	780	5	BP365835	BP365835	168	201	44.9	842	8	BT579756	BT579756
96	432	56.4	704	3	BP139064	BP139064	169	201	44.9	866	8	BT579756	BT579756
97	432	56.4	704	3	BP139064	BP139064	170	201	44.9	712	2	BT579756	BT579756
98	431	56.2	581	3	BP199948	BP199948	171	199.5	44.4	744	2	BT579756	BT579756
99	430	56.0	581	3	BP199948	BP199948	172	199	44.4	744	2	BT579756	BT579756
100	429	55.8	581	3	BP199948	BP199948	173	198.5	43.6	703	5	BT128677	BT128677
101	429	55.8	581	3	BP199948	BP199948	174	198.5	43.6	703	5	BT128677	BT128677
102	429	55.8	581	3	BP199948	BP199948	175	194.5	43.4	600	2	BT680090	BT680090
103	429	55.8	581	3	BP199948	BP199948	176	193.5	43.2	621	2	BT680090	BT680090
104	429	55.8	581	3	BP199948	BP199948	177	192	42.9	634	1	BT680090	BT680090
105	421	94.0	584	3	BP274942	BP274942	178	192	42.9	634	1	BT680090	BT680090
106	421	94.0	584	3	BP274942	BP274942	179	192	42.9	634	1	BT680090	BT680090
107	421	94.0	584	3	BP274942	BP274942	180	192	42.9	634	1	BT680090	BT680090
108	416	92.6	581	3	BP264149	BP264149	181	189	42.2	671	3	BT680090	BT680090
109	415	92.6	581	3	BP264149	BP264149	182	189	42.2	816	7	BT680090	BT680090
110	408	91.1	1090	7	BP264149	BP264149	183	189	42.2	927	6	BT680090	BT680090
111	405	90.4	915	5	BP264149	BP264149	184	185	41.3	519	2	BT680090	BT680090
112	401	89.5	922	5	BP264149	BP264149	185	184.5	41.2	425	6	BT680090	BT680090
113	401	89.5	922	5	BP264149	BP264149	186	182.5	40.7	1289	6	BT680090	BT680090
114	389	85.7	793	3	BP264149	BP264149	187	181.5	40.5	718	4	BT680090	BT680090
115	384	85.7	793	3	BP264149	BP264149	188	181	40.4	463	8	BT680090	BT680090
116	384	85.7	793	3	BP264149	BP264149	189	181	40.4	463	8	BT680090	BT680090
117	365	81.0	586	3	BP264149	BP264149	190	179.5	40.1	736	5	BT680090	BT680090
118	363	81.0	586	3	BP264149	BP264149	191	179	40.0	444	10	BT680090	BT680090
119	361	70.9	586	3	BP264149	BP264149	192	179	40.0	581	3	BT680090	BT680090
120	357	72.7	325	6	BP264149	BP264149	193	179	40.0	688	2	BT680090	BT680090
121	338	73.4	325	6	BP264149	BP264149	194	179	40.0	744	9	BT680090	BT680090
122	338	73.4	325	6	BP264149	BP264149	195	179	40.0	750	8	BT680090	BT680090
123	329	73.4	325	6	BP264149	BP264149	196	179	40.0	831	6	BT680090	BT680090
124	329	73.4	325	6	BP264149	BP264149	197	179	40.0	879	6	BT680090	BT680090
125	327	73.0	325	6	BP264149	BP264149	198	179	40.0	896	6	BT680090	BT680090
126	327	73.0	325	6	BP264149	BP264149	199	179	40.0	909	6	BT680090	BT680090
127	325	72.5	325	6	BP264149	BP264149	200	179	40.0	919	6	BT680090	BT680090
128	325	71.7	325	6	BP264149	BP264149	201	179	40.0	927	6	BT680090	BT680090
129	322	71.7	325	6	BP264149	BP264149	202	179	40.0	984	5	BT680090	BT680090
130	321	69.6	325	6	BP264149	BP264149	203	178.5	39.8	942	2	BT680090	BT680090
131	312	69.6	325	6	BP264149	BP264149	204	177	39.5	992	2	BT680090	BT680090
132	310	69.2	325	6	BP264149	BP264149	205	174	38.8	754	6	BT680090	BT680090
133	310	69.2	325	6	BP264149	BP264149	206	174	38.8	842	6	BT680090	BT680090
134	310	69.2	325	6	BP264149	BP264149	207	173	38.6	900	6	BT680090	BT680090
135	305	68.5	325	6	BP264149	BP264149	208	173	38.6	944	3	BT680090	BT680090
136	285	68.5	325	6	BP264149	BP264149	209	173	38.6	699	1	BT680090	BT680090
137	285	68.5	325	6	BP264149	BP264149	210	173	38.6	735	7	BT680090	BT680090
138	285	68.5	325	6	BP264149	BP264149	211	173	38.6	811	7	BT680090	BT680090
139	285	68.5	325	6	BP264149	BP264149	212	173	38.6	834	7	BT680090	BT680090
140	269	60.0	635	2	BP264149	BP264149	213	173	38.6	838	7	BT680090	BT680090
141	269	60.0	635	2	BP264149	BP264149	214	173	38.6	846	7	BT680090	BT680090
142	229	51.1	645	2	BP264149	BP264149	215	173	38.6	857	7	BT680090	BT680090
143	229	51.1	645	2	BP264149	BP264149	216	173	38.6	857	7	BT680090	BT680090
144	220	49.1	625	5	BP264149	BP264149	217	160.5	37.3	827	8	BT680090	BT680090
145	220	49.1	625	5	BP264149	BP264149	218	160.5	37.3	827	8	BT680090	BT680090
146	219.5	48.0	625	5	BP264149	BP264149	219	165	36.8	491	1	BT680090	BT680090
147	217.5	48.4	600	2	BP264149	BP264149	220	165	36.8	1236	8	BT680090	BT680090
148	217	48.4	577	9	BP264149	BP264149	221	164	36.6	544	1	BT680090	BT680090
149	213.5	47.4	549	7	BP264149	BP264149	222	162	36.2	666	7	BT680090	BT680090
150	212.5	47.4	531	7	BP264149	BP264149	223	160.5	35.8	611	2	BT680090	BT680090
151	212.5	47.4	531	7	BP264149	BP264149	224	156.5	34.9	634	5	BT680090	BT680090
152	212.5	47.4	531	7	BP264149	BP264149	225	156.5	34.9	634	5	BT680090	BT680090
153	212.5	47.4	531	7	BP264149	BP264149	226	156	34.8	547	1	BT680090	BT680090

C	227	155	34.6	570	5	BU976761	603534313	C	300	96	21.4	568	1	AL727624	AL727624
C	228	153.5	34.3	847	8	DR8677246	JGI_CABG9		301	96	21.4	729	1	DR704222	DR704222
C	229	153	34.2	304	2	BE619103	BE619103		302	94.5	21.1	441	7	CN807482	CN807482
C	230	153	34.2	312	3	BH153209	TCBAP1Q4		303	94	21.0	149	3	BQ336306	BQ336306
C	231	153	34.2	480	6	CA777140	IP03Ef10.Y		304	94	21.0	746	2	BF140146	BF140146
C	232	153	34.2	582	3	BP194502	BP194502		305	92.5	20.6	193	1	AA163045	AA163045
C	233	153	34.2	685	7	CK981492	CK981492		306	92.5	20.6	1174	6	CD509260	CD509260
C	234	153	34.2	722	2	BF679649	BF679649		307	92	20.5	373	5	AL398593	AL398593
C	235	153	34.2	782	7	CO918949	AGENCOURT		308	91	20.3	379	5	EY038773	EY038773
C	236	150.5	33.6	802	8	DN100293	JGI_CABE8		309	90	20.1	260	11	TSF458761	TSF458761
C	237	150.5	33.6	835	8	CX937110	JGI_CAOS		310	89	19.9	961	8	DR946006	DR946006
C	238	149.5	33.4	456	1	AA839622	wv9Teo6.r		311	87.5	19.5	918	2	BF992133	BF992133
C	239	148.5	33.1	757	10	BK198893	Danilo_rer		312	87	19.4	313	2	CV740501	CV740501
C	240	147.5	32.9	525	2	BE290901	601084205		313	86.5	19.3	723	7	CV740501	CV740501
C	241	145.5	32.5	675	1	AL722584	AL722584		314	86.5	19.3	730	7	CV756544	CV756544
C	242	145.5	32.5	827	5	BQ443284	UT-M-EV0-		315	86.5	19.3	809	8	CX863267	CX863267
C	243	145	32.4	537	7	CR774766	KFE2Pd69A		316	86.5	19.3	1453	4	AY814979	AY814979
C	244	144	32.1	991	1	AL879624	AL879624		317	86	19.2	361	5	BY020675	BY020675
C	245	143.5	32.0	891	5	BK780455	BK780455		318	85.5	19.1	654	6	CD321260	CD321260
C	246	143.5	32.0	799	1	AM199574	AM199574		319	85	19.0	654	8	CX682762	CX682762
C	247	140.5	31.4	672	11	DE094838	daosf507.Y		320	84.5	18.9	880	9	BH207435	BH207435
C	248	140.5	31.4	894	5	BK776016	DE094838_Oryzias_1		321	83.5	18.6	586	3	BT898841	BT898841
C	249	137	30.6	563	8	DR003404	TCI14160		322	83	18.5	581	3	BE262101	BE262101
C	250	136.5	30.5	352	6	CB780491	AMGNNUC:N		323	83	18.5	983	2	BF337260	BF337260
C	251	136	30.4	1030	5	BU235217	603791177		324	82	18.3	369	5	BY101168	BY101168
C	252	134	29.9	297	2	BF170990	PCL1883.M		325	82	18.3	448	1	AI208756	AI208756
C	253	131	29.2	860	8	CX958090	JGI_CAOA9		326	82	18.3	463	2	BF893919	BF893919
C	254	127.5	28.5	808	8	DN932266	AGENCOURT		327	82	18.3	484	3	BI424242	BI424242
C	255	125	27.9	454	2	BG982031	MK3-CN014		328	82	18.3	552	5	BU080681	BU080681
C	256	124.5	27.8	839	5	BX911124	BX911124		329	82	18.3	558	3	EM885374	EM885374
C	257	124	27.7	623	1	AL725543	EX911124		330	82	18.3	903	6	CF712017	CF712017
C	258	123.5	27.6	424	4	AK180792	Mus_muscu		331	82	18.3	920	2	BF526774	BF526774
C	259	123	27.5	760	5	BU204728	604152621		332	81.5	18.2	364	1	AA982672	AA982672
C	260	122	27.2	463	2	BF852284	MK3-EN008		333	81.5	18.2	416	2	BE624685	BE624685
C	261	120	26.8	156	3	BO331200	MR4-ET001		334	81.5	18.2	567	3	BP049364	BP049364
C	262	120	26.8	296	2	BG982036	MR3-CN014		335	81.5	18.2	624	1	AA536675	AA536675
C	263	120	26.8	422	2	BG982044	MR3-CN014		336	81.5	18.2	676	6	CF743564	CF743564
C	264	120	26.8	435	3	BO332331	MR4-ET014		337	81.5	18.2	682	10	CZ905189	CZ905189
C	265	120	26.8	437	2	BF768820	PMO-IT001		338	81.5	18.2	886	5	BU050745	BU050745
C	266	120	26.8	440	2	BG982029	MR3-CN014		339	81	18.1	1012	6	CB209613	CB209613
C	267	120	26.8	440	2	BG982036	MR3-CN014		340	80.5	18.0	468	3	BI317492	BI317492
C	268	120	26.8	453	2	BF773259	PMO-IT001		341	80	17.9	665	7	CV249386	CV249386
C	269	120	26.8	453	3	BO315535	PMO-IT001		342	80	17.9	695	7	CV246027	CV246027
C	270	120	26.8	456	2	BF996800	OV3-GN020		343	80	17.9	706	9	CV250470	CV250470
C	271	120	26.8	459	2	BG982034	MR3-CN014		344	80	17.9	810	9	CC477031	CC477031
C	272	120	26.8	461	2	BG982012	MR3-CN014		345	79.5	17.7	487	3	BI443444	BI443444
C	273	120	26.8	479	2	BF997052	OV3-GN020		346	79.5	17.7	651	5	BO852542	BO852542
C	274	119	26.6	247	2	BF768814	PMO-IT001		347	79.5	17.7	711	5	BO995001	BO995001
C	275	119	26.6	460	2	BF693150	PM1-MT014		348	79.5	17.7	744	8	DR950944	DR950944
C	276	117	26.1	134	3	BO61261	BO61261		349	79.5	17.7	797	8	CX863376	CX863376
C	277	117	26.1	441	2	BF893925	PM1-MT014		350	79.5	17.7	904	8	DR939601	DR939601
C	278	116.5	26.0	410	2	BG091909	fmac18c11.		351	79.5	17.7	926	8	DR929708	DR929708
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C	280	116	25.9	574	3	BI445352	MA		353	79	17.6	476	8	DT071039	DT071039
C	281	116	25.9	640	6	CB505136	sasaplhb5		354	78.5	17.5	420	4	CNS0CG3F	CNS0CG3F
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Thu Mar 16 10:39:27 2006

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Page 4

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394	78	17.4	989	5	BO676384	BO676384	BO676384	BO676384	467	74	16.5	652	7	CK181784	EST771104	CK181784	EST771104
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ALIGNMENTS

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Hominidae; Homo
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Melton D., Brown J., Kenny G., Permutt A., Lee C., Kaestner K.,
Lentgha T., Scarce M., Brestelli J., Gadowol J., Clifton S.,
Hillier A., Warren M., Pape D., Wylie T., Martin J., Blaisdell A.,
Schiller A., Theising B., Rutter E., Ronko I., Bennett J.,
Cargnani M., Gibbons M., McCann R., Cole R., Teagarden W., R.,
Williams M., Jackson Y., and Bowers Y.
Unpublished (2000)
Unpublished 112c11.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
```

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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@hms.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on:1.edu
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco.

FEATURES

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XhoI; Site 2: EcoRI; Constructed with lambda Zapri system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine Box
8127, 660 S Euclid Ave, St. Louis, MO 63110. Note: this
is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
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US-10-757-745-2_COPY_54_140 (1-87) x BQ582059 (1-429)

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RESULT 2
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VERSION CR543841
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pongo.
1 (bases 1 to 471)
Bloeker, H., Boecker, M., Brandt, P., Mewes, H. W., Well, B., Amid, C., Oanger, A., Fob, G., Han, M. and Wiemann, S., Brandt, P., et al.)
Pongo pygmaeus mRNA (Bloeker, H., Boecker, M., Brandt, P., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by GSF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany)
Within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp45900742) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

FEATURES
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/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN
Alignment Scores:
Pred. No.: 6.69e-47 Length: 471
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR543841 (1-471)

QY 1 MetGluArgAlaLeuAnSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 161 ATGGAAGAGGCTGTGAACCTCTACTTCGAGCCTCCGGTGAGAGAGCCCTTGGAACGC 220
QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
Db 221 CGCCCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAAGAAACACT 280
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 281 GATTCACACCATCTTAAATCAACCCATCTGAAGATCTCAAGCAAGAAATGACAGCATG 340
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 341 TTCTCTCATTAACCTGGAATATGATGATTGATTAACATCATCTGCAGAGAGGCT 400
QY 81 ArgGlyValCysSerTyrLeu 87
Db 401 CGAGGGGTGTGTCTACTTA 421
RESULT 3
LOCUS CB120234 473 bp mRNA linear EST 28-JAN-2003
DEFINITION K-EST0167337 LBSCKO Homo sapiens cDNA clone LBSCKO-29-F06 5', mRNA
sequence.
ACCESSION CB120234
VERSION CB120234.1 GI:27946036
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 473)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.U., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-353, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29 row: F column: 06
High quality sequence stop: 473.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LBSCKO-29-F06"
/sex="M"
/cell_line="SCK"
/lab_host="Top10P"
/clone_idb="LBSCKO"
/note="Organ: Liver; Vector: pT73-Pac; Site_1: EcoRI; Site_2: NotI; The library was contributed by the Soares Laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

FEATURES
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/mol_type="mRNA"
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/lab_host="Top10P"
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ORIGIN
Alignment Scores:
Pred. No.: 6.73e-47 Length: 473
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CB120234 (1-473)

QY 1 MetGluArgAlaLeuAnSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
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QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
Db 169 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAAGAAACACT 228
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 229 GATTCACACCATCTTAAATCAACCCATCTGAAGATCTCAAGCAAGAAATGACAGCATG 288
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 289 TTCTCTCATTAACCTGGAATATGATGATTGATTAACATCATCTGCAGAGAGGCT 348
QY 81 ArgGlyValCysSerTyrLeu 87
Db 349 CGAGGGGTGTGTCTACTTA 369
RESULT 4
LOCUS AT750554 480 bp mRNA linear EST 20-JUN-2002
DEFINITION cl04a01.y1 Normal Human Triaecular Bone Cells Homo sapiens cDNA
clone NHTBC_cl04a01 random, mRNA sequence.
ACCESSION AT750554

VERSION AT750554.1 GI:5128918
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 480)
Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G., Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.T., Yang, L.M., Robey, P.G., Hotchkiss, R.N., and Francomano, C.A.
SGAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
JOURNAL Contact: Libin Jia
COMMENT Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).
Plate: 04 Row: A Column: 01
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
source 1..480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NHTBC_c04a01"
/sex="Female"
/tissue_type="Bone"
/cell_type="Tribecular Bone Cells"
/lab_host="SURE"
/clone_idb="Normal Human Tribecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site: 1; EcorI; Library constructed by Dr. Marian Young and Dr. Pamela Gehron Robey (NIDCR)"
ORIGIN
Alignment Scores:
Pred. No.: 6.86e-47 Length: 480
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 1
US-10-757-745-2_COPY_54_140 (1-87) x AT750554 (1-480)
QY 1 MetGluArgAlaLeuAuaenSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
Db 154 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGGAGAGCGCTTGGAAAGC 213
QY 21 ArgProGluThrIleSerGluProGlyThrTyValAspLeuThrAngGluGluThr 40
Db 214 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACTTAACCAATGAGAAACAAC 273
QY 41 AAsPserThrTrpSerIleSerProSerGluAAsPThrGlnGlnGluAngIYSerMet 60
Db 274 GATTCACCACTCTTAATAATCAGCCCTCTGAAGATCTCAGCAAGAAATGGCAGCATG 333
QY 61 PheSerLeuIleThrTPAAsIleAspGlyLeuAAsPLeuAAsnAAsnLeuSerGluArgAla 80
Db 334 TTCTCTCATTAACCTGGAATATGATGATTGATTCATTAACAATCTGTCAGAGAGGCT 393
QY 81 ArgGlyValCysSerTyLeu 87
Db 394 CGAGGGGTGTGTTCTACTTA 414
RESULT 5
AA486032
LOCUS AA486032 485 bp mRNA linear EST 06-MAR-1998

DEFINITION ab40b10.r1 Stratagene Hela cell s3 937216 Homo sapiens CDNA clone
IMAGE:843259 5', mRNA sequence.
ACCESSION AA486032
VERSION AA486032.1 GI:2216248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 485)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S., Kitzman, D., Kucada, T., Lacy, M., Le, N., Lennon, G., Matis, M., Martin, V., Moore, B., Schellberg, R., Stepcie, M., Tan, F., Theisberg, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI Human EST Project
Unpublished (1997)
JOURNAL Contact: Wilson R.
COMMENT Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: set@watson.wustl.edu
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1913 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 444.
Location/Qualifiers
source 1..485
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/db_xref="taxon:9606"
/clone="IMAGE:843259"
/sex="Female"
/dev_stage="Hela S3 cell line"
/lab_host="GOLR (kanamycin resistant)"
/clone_idb="Stratagene Hela cell s3 937216"
/note="Vector: pBluescript SK-; Site: 1; EcorI; Site: 2; XhoI; Cloned unidirectionally. Primer: 0190 dt. Hela S3 epithelioid carcinoma cells grown to semi-confluency without induction. Average insert size: 1.5 kb; Uni-ZAP XR Vector. ~5' adaptor sequence: 5' GATTCGCGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."
ORIGIN
Alignment Scores:
Pred. No.: 6.95e-47 Length: 485
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 1
US-10-757-745-2_COPY_54_140 (1-87) x AA486032 (1-485)
QY 1 MetGluArgAlaLeuAuaenSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
Db 150 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAAGC 209
QY 21 ArgProGluThrIleSerGluProGlyThrTyValAspLeuThrAngGluGluThr 40
Db 210 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACTTAACCAATGAGAAACAAC 269
QY 41 AAsPserThrTrpSerIleSerProSerGluAAsPThrGlnGlnGluAngIYSerMet 60
Db 270 GATTCACCACTCTTAATAATCAGCCCTCTGAAGATCTCAGCAAGAAATGGCAGCATG 329
QY 61 PheSerLeuIleThrTPAAsIleAspGlyLeuAAsPLeuAAsnAAsnLeuSerGluArgAla 80
Db 330 TTCTCTCATTAACCTGGAATATGATGATTGATTCATTAACAATCTGTCAGAGAGGCT 389
QY 81 ArgGlyValCysSerTyLeu 87

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.tbl

Page 12

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QY 61 PheSerIeu1leThrTPAsn1leAspGlyLeuAspLeuAsn1leuSerGluArgAla 80
DB 249 TTCTCTCTCATTAACCTGGAATATTGATGATAGATCTAAACAATCTGTCTGAGAGGGCT 308
QY 81 ArgGlyValCysSerTyrLeu 87
DB 309 CGAGGGGTGTGTCTCTACTTA 329

RESULT 8
BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
LOCUS BP226620 565 bp mRNA linear EST 15-SEP-2004
DEFINITION clone DMC03190, mRNA sequence.
ACCESSION BP226620
VERSION BP226620.1 GI:52099525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 565)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15442556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
source 1..565
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DMC03190"
/clone_lib="Sugano cDNA library, dermoid cancer"
/note="dermoid cancer"

ORIGIN
Alignment Scores:
Pred. No.: 8,49e-47 Length: 565
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP226620 (1-565)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 161 ATGGAAGGGCTCTGAACCTCTCACTTCGAGCTCCGCGAGGAGAGCGCTTGGAAGCG 220
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 221 CGACCTGAAACCACTCTGAGCCCAAGCACTATGTTGACCTTAACAATGAGAAACAAT 280
QY 41 AspSerThrThrseryIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 281 GATTCACCACTCTTAAATCAAGCCATCTGAAGTCACTCAAGCAAGAAATGCAACAG 340
QY 61 PheSerIeu1leThrTPAsn1leAspGlyLeuAspLeuAsn1leuSerGluArgAla 80
DB 341 TTCTCTCTCATTAACCTGGAATATTGATGATAGATCTAAACAATCTGTCTGAGAGGGCT 400
QY 81 ArgGlyValCysSerTyrLeu 87
DB 401 CGAGGGGTGTGTCTCTACTTA 421
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RESULT 9
BP220508 Sugano cDNA library, colon Homo sapiens cDNA clone
LOCUS BP220508 566 bp mRNA linear EST 15-SEP-2004
DEFINITION COL03160, mRNA sequence.
ACCESSION BP220508
VERSION BP220508.1 GI:52093413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 566)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
source 1..566
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/db_xref="taxon:9606"
/clone="COL03160"
/tissue_type="colon"
/clone_lib="Sugano cDNA library, colon"

ORIGIN
Alignment Scores:
Pred. No.: 8,51e-47 Length: 566
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP220508 (1-566)
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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 139 CGACCTGAAACCACTCTGAGCCCAAGCACTATGTTGACCTTAACAATGAGAAACAAT 198
QY 41 AspSerThrThrseryIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 199 GATTCACCACTCTTAAATCAAGCCATCTGAAGTCACTCAAGCAAGAAATGCAACAG 258
QY 61 PheSerIeu1leThrTPAsn1leAspGlyLeuAspLeuAsn1leuSerGluArgAla 80
DB 259 TTCTCTCTCATTAACCTGGAATATTGATGATAGATCTAAACAATCTGTCTGAGAGGGCT 318
QY 81 ArgGlyValCysSerTyrLeu 87
DB 319 CGAGGGGTGTGTCTCTACTTA 339

RESULT 10
BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone
LOCUS BP257211 568 bp mRNA linear EST 16-SEP-2004
DEFINITION HRT00430, mRNA sequence.
ACCESSION BP257211
VERSION BP257211.1 GI:52172441
KEYWORDS EST.
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SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN	ALIGNMENT SCORES:	US-10-757-745-2_COPY_54_140' (1-87) * BP257211 (1-568)
ORGANISM	Homo sapiens (human)								
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 568)							
REFERENCE	Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.								
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions								
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)								
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp.								
FEATURES	Location/Qualifiers								
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	/db_xref="taxon:9606"								
	/clone="HRT00430"								
	/cisseue_type="heart"								
	/clone_lib="Sugano cDNA library, heart"								
ALIGNMENT SCORES:									
Pred. No.:	8,55e-47	Length:	568						
Score:	448.00	Matches:	87						
Percent Similarity:	100.0%	Conservative:	0						
Best Local Similarity:	100.0%	Mismatches:	0						
Query Match:	100.0%	Indels:	0						
DB:	3	Gaps:	0						
US-10-757-745-2_COPY_54_140' (1-87) * BP257211 (1-568)									
QY	1 MetGuaAgaAlaLeuasnSerTyrrheGluProProValGluGluSerAlaLeuGluAa 20								
DB	130 ATGGAAGAGGGCTCTGAACTCTCACTTCAGAGCTCCGGTGAAGAGAGCGCTTGAAACGC 189								
QY	21 ArpProGluThrIleSerGluProIyrrhTyrrValaApleuThraAngGluGluThr 40								
DB	190 CGACCTGAACCAATCTCTGAGCCCAAGACCTATGTGACCTPAACCAATGAAGAAACAAC 249								
QY	41 AapSerThrTrSerIleSerProSerGluAepThrGluGluGluGluGluGluGlu 60								
DB	250 GATTCACACCACTTCAAAATGACGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCAT 309								
QY	61 PheSerIleuIleThrTyraenIleAepGlyLeuApleuAenAenIleSerGluAa 80								
DB	310 TTCTCTCATTAATCTGGAATTAATGATGATTAAGTCAACCAATCTGTCAAGAGGCT 369								
QY	81 ArgGlyValCySerTyrrLeu 87								
DB	370 CGAGGCGGTGTCTCTACTTA 390								
RESULT 11									
BP221518									
LOCUS	BP221518 Sugano cDNA library, colon Homo sapiens cDNA clone	570 bp	mRNA	linear	EST 15-SEP-2004				
DEFINITION	CCO09203, mRNA sequence.								
ACCESSION	BP221518								
VERSION	BP221518.1 GI:52094423								
KEYWORDS	EST.								
SOURCE	Homo sapiens (human)								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.								
REFERENCE	1 (bases 1 to 570)								
AUTHORS	Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.								

TITLE	SEQUENCE COMPARISON OF HUMAN AND MOUSE GENES REVEALS A HOMOLOGOUS BLOCK STRUCTURE IN THE PROMOTER REGIONS
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)
PUBMED	15342556
CONTACT	Contact: Yutaka Suzuki
DEPARTMENT	Department of Virology
INSTITUTE	Institute of Medical Science, University of Tokyo
ADDRESS	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
EMAIL	Email: yusuzuki@ims.u-tokyo.ac.jp.
LOCATION	Location/Qualifiers
1. 570	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="COL09203"	
/issue_type="colon"	
/clone_id="sugano cdna library, colon"	
ALIGNMENT SCORES:	
Pred. No.:	8.59e-47
Score:	448.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	3
US-10-757-745-2_COPY_54_140 (1-87) x BP221518 (1-570)	
QY	1 MetGluArgAlaLeuAuaSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB	68 ATGAAAAGGGCTCGAAGCTCTACTTGAAGCTCGGTGAGAGAGACGCTTGAAAGC 127
QY	21 ArgProGluThrIleSerGluProIleGlyThrTyrAlaIlePheLeuThrArgGluThrThr 40
DB	128 CGACCTGAACCACTCTCGAGCCCAAGACCTATGTACCTAACCAATGAAGAAACAAC 187
QY	41 AspSerThrThrSerIleSerIleSerProSerGluAspThrGluGluGluGluGluGluSerMet 60
DB	188 GATTCACACACTTCTTAATATCAGCCCATCTGAAGATCTACGACAAAGAAATGCGAGATG 247
QY	61 PheSerLeuIleThrTTPaenIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB	248 TTCTCTCTCACTTACTGGAATATGATGATTAACAATCTGTGAGAGAGGCT 307
QY	81 ArgGlyValCysSerTyrLeu 87
DB	308 CGAGGGGTGTCTTCTTACTTA 328
RESULT 12	
LOCUS	AU279894
DEFINITION	AU279894 CHONS2 Homo sapiens cdna clone CHONS2002038 5', mRNA
ACCESSION	AU279894
VERSION	AU279894.1
KEYWORDS	GI:28299121
ORGANISM	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
ORGANISM	Hominiidae; Homo.
ORGANISM	1 (bases 1 to 573)
ORGANISM	Imabayashi,H., Mori,T., Gojo,S., Kiyono,T., Sugiyama,T., Irie,R.,
ORGANISM	Isogai,T., Hata,J., Tomoya,Y., and Umezawa,A.
ORGANISM	Redifferentiation of dedifferentiated chondrocytes and
ORGANISM	chondrogenesis of human bone marrow stromal cells via chondrosphere
ORGANISM	formation with expression profiling by large-scale cDNA analysis
ORGANISM	Exp. Cell Res. 288 (1), 35-50 (2003)
ORGANISM	12878157
ORGANISM	Contact: Takao Isogai
ORGANISM	Genomics Laboratory
ORGANISM	Helix Research Institute

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ORIGIN /cissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

Alignment Scores:

Pred. No.: 8,65e-47 Length: 573
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP262642 (1-573)

QY 1 MetGluAArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 66 ATGGAAAGGGCTGTGAACCTCTAATCGAGCCCTCCGTGAGAGAGAGCCCTTGGAAACCC 125
QY 21 ATGProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 126 CACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAAGAACACT 185
QY 41 AAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 186 GATTCACACCATCTCTAAATATGAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 245
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 246 TTCTCTCATTAACCTGAATATGATGATTAGATCAATCAATCTGTGAGAGAGGCT 305
QY 81 ArgGlyValCysSerTyrLeu 87
DB 306 CGAGGGGTGTGTCTTACTTA 326

RESULT 15

BP262642 576 bp mRNA linear EST 16-SEP-2004
LOCUS BP262642 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS107584, mRNA sequence.

ACCESSION BP262642 GI:52177873
VERSION BP262642.1
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

AUTHORS 1 (bases 1 to 576)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL

PUBMED

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source 1..576
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HS107584"
/cissue_type="small intestine"
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ORIGIN

Alignment Scores:
Pred. No.: 8,71e-47 Length: 576
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP262642 (1-576)

QY 1 MetGluAArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 84 ATGGAAAGGGCTGTGAACCTCTAATCGAGCCCTCCGTGAGAGAGAGCCCTTGGAAACCC 143
QY 21 ATGProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 144 CACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAAGAACACT 203
QY 41 AAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 204 GATTCACACCATCTCTAAATATGAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 263
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 264 TTCTCTCATTAACCTGAATATGATGATTAGATCAATCAATCTGTGAGAGAGGCT 323
QY 81 ArgGlyValCysSerTyrLeu 87
DB 324 CGAGGGGTGTGTCTTACTTA 344

RESULT 16

CN298919 577 bp mRNA linear EST 16-MAY-2004
LOCUS CN298919 1700600175228 GRN_PPREHP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN298919
ACCESSION CN298919 GI:4731533
VERSION CN298919.1
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo

AUTHORS

1 (bases 1 to 577)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,
Lebkoweki, J. and Stanton, L.W.

TITLE Transcriptionome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA

TELE: 650 473 8658
FAX: 650 473 7760
Email: rbrandenberger@geron.com

Insert Length: 577 Std Error: 0.00.
location/Qualifiers

FEATURES

source 1..577
/organism="Homo sapiens"
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/cissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PPREHP"
/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated h9 cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 8,73e-47 Length: 577
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CN298919 (1-577)

Qy 1 MetGUARGAlaAuaAnSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
 Db 160 ATGGAAGGGCTCTGAACCTCTTACTTGAGCCCTCCGGTGGAGAGAGCGCTTGGAACCC 219

Qy 21 ArgProGluThrIleSerGluProValThyValAspLeuThrAsnGluGluThrThr 40
 Db 220 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACACT 279

Qy 41 AspSerThrSerIleSerProSerGluAspThrGluGluGluGluGluSerMet 60
 Db 280 GATTCACCACTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 339

Qy 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
 Db 340 TTCTCTCATTAAGTGAATATGATGATGATGATCTAACATCTGTCAGAGAGGCT 399

Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 400 CGAGGGGTGTCTTCTACTTA 420

RESULT 17
 BP274368 580 bp mRNA linear EST 16-SEP-2004
 LOCUS BP274368 Sugano cDNA library, kidney Homo sapiens cDNA clone
 DEFINITION K0N00894. mRNA sequence.

ACCESSION BP274368
 VERSION BP274368.1 GI:52188100
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 580)
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ms.u-tokyo.ac.jp.

FEATURES
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 1..580
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="K0N00894"
 /issue_type="kidney"
 /clone_lib="Sugano cDNA library, kidney"

ORIGIN
 Alignment Scores: 8.79e-47 Length: 580
 Pred. No.: 448.00 Matches: 87
 Score: 448.00 Conservative: 0
 Percent Similarity: 100.0% Mismatches: 0
 Best Local Similarity: 100.0% Indels: 0
 Query Match: 100.0% Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP274368 (1-580)

Qy 1 MetGUARGAlaAuaAnSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
 Db 180 ATGGAAGGGCTCTGAACCTCTTACTTGAGCCCTCCGGTGGAGAGAGCGCTTGGAACCC 239

Qy 21 ArgProGluThrIleSerGluProValThyValAspLeuThrAsnGluGluThrThr 40
 Db 240 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACACT 299

Qy 41 AspSerThrSerIleSerProSerGluAspThrGluGluGluGluGluSerMet 60
 Db 300 GATTCACCACTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 359

Qy 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
 Db 360 TTCTCTCATTAAGTGAATATGATGATGATGATCTAACATCTGTCAGAGAGGCT 419

Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 420 CGAGGGGTGTCTTCTACTTA 440

RESULT 18
 BP207751 581 bp mRNA linear EST 14-SEP-2004
 LOCUS BP207751 Sugano cDNA library, coronary artery smooth muscle cell
 DEFINITION Homo sapiens cDNA clone CASH1735, mRNA sequence.

ACCESSION BP207751
 VERSION BP207751.1 GI:52064157
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 581)
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ms.u-tokyo.ac.jp.

FEATURES
 source
 1..581
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CASH1735"
 /issue_type="coronary artery"
 /cell_type="smooth muscle cell"
 /clone_lib="Sugano cDNA library, coronary artery smooth
 muscle cell"

ORIGIN
 Alignment Scores: 8.81e-47 Length: 581
 Pred. No.: 448.00 Matches: 87
 Score: 448.00 Conservative: 0
 Percent Similarity: 100.0% Mismatches: 0
 Best Local Similarity: 100.0% Indels: 0
 Query Match: 100.0% Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP207751 (1-581)

Qy 1 MetGUARGAlaAuaAnSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
 Db 68 ATGGAAGGGCTCTGAACCTCTTACTTGAGCCCTCCGGTGGAGAGAGCGCTTGGAACCC 127

Qy 21 ArgProGluThrIleSerGluProValThyValAspLeuThrAsnGluGluThrThr 40
 Db 128 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACACT 167

Qy 41 AspSerThrSerIleSerProSerGluAspThrGluGluGluGluGluSerMet 60

Db 188 GATTCACCACTTCTAATAATGACCCATCTGAAGATCTACAGAGAATAATGGACGAC 247
QY 61 PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGIuArgAla 80
Db 248 TTCTCTCATTAACCTGGAATATGATGATTAGATTAAACAATCTGTCCAGAGAGGGCT 307
QY 81 ArgGIValCySeSerTyrLeu 87
Db 308 CGAGGGGTGTCTTCTACTTA 328

RESULT 19

BP225088

LOCUS BP225088 Sugano cDNA library, lymphocyte Daudi Homo sapiens cDNA
DEFINITION BP225088 Sugano cDNA library, lymphocyte Daudi Homo sapiens cDNA
clone DAT05184, mRNA sequence.

ACCESSION BP225088

VERSION BP225088.1 GI:52097993

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE 1 (bases 1 to 581)

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT PUBMED 15342556

CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.FEATURES
source Location/Qualifiers
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DAT05184"
/cell_type="lymphocyte"
/cell_line="Daudi"
/clone_lib="Sugano cDNA library, lymphocyte Daudi"
/note="Burkitt's lymphoma"

ORIGIN

Alignment Scores:
Pred. No.: 8,81e-47 Length: 581
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3

US-10-757-745-2_COPY_54_140 (1-87) x BP225088 (1-581)
QY 1 MetGIuArgAlaLeuAsnSerTyrPheGIuProProValGIuGIuSerAlaLeuGIuArg 20
Db 181 ATGGAAGGGCTCTGAACCTCTAATCGAGCTCCGGTGAGAGAGCCCTTGGAGACGC 240
QY 21 ArgPProGIuThrIleSerGIuProIleThrTyrValAspLeuThrAsnGIuGIuThr 40
Db 241 GAACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAACCT 300
QY 41 AepSerThrThrSerIleSerProSerGIuAspThrGIuGIuAsnGIuSerMet 60
Db 301 GATTCACCACTTCTAATAATGACCCATCTGAAGATCTACAGAGAATAATGGACGAC 360
QY 61 PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGIuArgAla 80
Db 361 TTCTCTCATTAACCTGGAATATGATGATTAGATTAAACAATCTGTCCAGAGAGGGCT 420

QY 81 ArgGIValCySeSerTyrLeu 87
Db 421 CGAGGGGTGTCTTCTACTTA 441

RESULT 20

BP262638

LOCUS BP262638 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION BP262638 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS107576, mRNA sequence.

ACCESSION BP262638

VERSION BP262638.1 GI:52177869

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE 1 (bases 1 to 581)

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT PUBMED 15342556

CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.FEATURES
source Location/Qualifiers
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS107576"
/tissue="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN
Alignment Scores:
Pred. No.: 8,81e-47 Length: 581
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3

US-10-757-745-2_COPY_54_140 (1-87) x BP262638 (1-581)
QY 1 MetGIuArgAlaLeuAsnSerTyrPheGIuProProValGIuGIuSerAlaLeuGIuArg 20
Db 77 ATGGAAGGGCTCTGAACCTCTAATCGAGCTCCGGTGAGAGAGCCCTTGGAGACGC 136
QY 21 ArgPProGIuThrIleSerGIuProIleThrTyrValAspLeuThrAsnGIuGIuThr 40
Db 137 GAACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAACCT 196
QY 41 AepSerThrThrSerIleSerProSerGIuAspThrGIuGIuAsnGIuSerMet 60
Db 197 GATTCACCACTTCTAATAATGACCCATCTGAAGATCTACAGAGAATAATGGACGAC 256
QY 61 PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGIuArgAla 80
Db 257 TTCTCTCATTAACCTGGAATATGATGATTAGATTAAACAATCTGTCCAGAGAGGGCT 316

QY 81 ArgGIValCySeSerTyrLeu 87
Db 317 CGAGGGGTGTCTTCTACTTA 337

RESULT 21

BP270744

LOCUS BP270744 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION BP270744 Sugano cDNA library, small intestine Homo sapiens cDNA

ACCESSION	clone KAR05146, mRNA sequence.
VERSION	BP270744
KEYWORDS	BP270744.1 GI:52220093
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Kukuryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
AUTHORS	1 (bases 1 to 581)
TITLE	Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
JOURNAL	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
PUBMED	Genome Res. 14 (9), 1711-1718 (2004)
COMMENT	15342556 Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8659, Japan Email: yusuzuki@ime.u-tokyo.ac.jp
FEATURES	Location/Qualifiers
source	1..581 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="KAR05146" /tissue_type="small intestine" /clone_lib="Sugano cDNA library, small intestine"
ALIGNMENT	Alignment Scores:
Pred. No.:	8,81e-47 Length: 581
Score:	448.00 Matches: 87
Percent Similarity:	100.0% Conservative: 0
Best local Similarity:	100.0% Mismatches: 0
Query Match:	100.0% Indels: 0
DB:	Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP270744 (1-581)	
OY	1 MetGUAAGAlaleuamserYrPhedLpProPrVAlGluGuseAAlaengLwag 20
DB	68 ATGGAAAGGCTCTGAACCTCTACTCTCAAGCTCCGATGGAGAGGCGCTTGGAAC 127
OY	21' ArgPrvoglUmrLleSerGluPrvolyrThrTyValAspleuThaengGluGlyrThr 40
DB	128 CCACTGAAACCATCTCTAGCCCAAGCACTATGTGATCTTACCAACAAGAAACAACT 187
OY	41 AapSerThrSerLygAlleSeProSerGluAspThrGlnGlnGluAengLyserMet 60
DB	188 GATTCACACACTCTTAAATCTCAACCACTCTAACAATCTCAAGAAATGGAGATG 247
OY	61 BheSerIuellerThrThpantlleApolyLeuAspleuAsnAsnLeuSerGluArgAla 80
DB	248 TTCCTCTCATTTACTAGAAATATATGATGATTTAAATCAATCTCTCAGAGAGGCT 307
OY	81 ArgGlyValCysSerTyrlen 87
DB	308 CCAAGGAGGTGTCTCTACTTA 328
RESULT 22	
LOCUS	BP379659 561 bp mRNA linear EST 21-SEP-2004
DEFINITION	BP379659 Sugano cDNA library, uterus Homo sapiens cDNA clone
ACCESSION	WMD06642, mRNA sequence.
VERSION	BP379659
KEYWORDS	BP379659.1 GI:52412762
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE	Hominidae; Homo.
AUTHORS	1 (bases 1 to 581)
TITLE	Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
JOURNAL	Mitsuhama-Sugano,J., Nakai,K. and Sugano,S.
PIUMED	Sequence comparison of human and mouse genes reveals a homologous
COMMENT	block structure in the promoter regions
	Genome Res. 14 (9), 1711-1718 (2004)
	15342556
	Contact: Yutaka Suzuki.
	Department of Virology
	Institute of Medical Science, University of Tokyo
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
	Email: yensuki@ims.u-tokyo.ac.jp.
FEATURES	Location/Qualifiers
source	1..581
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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="WMD06642"
	/issue_type="uternus"
ORIGIN	/clone_lib="Sugano cDNA library, uternus"
Alignment Scores:	
Prod. No.:	8..81e-47
Score:	448.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	3
	Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP379659 (1-581)	
Qy	1 Metctatgagatataaataaagcttctgphgclupropovaglugiugiserlatatengluary 20
Db	69 ATGGAAGAGGCTCTAATCTCTACTTCTGAGCTCCGATGAGAGAGAGCCGCTTGAGAGCC 128
Qy	21 ArgproglutthrltaseccluproltythrtyrValaaaplutPrtaangluglunthr 40
Db	129 GCACTTAAACATCTCTGAGCCCAAGACCTATGTTGACCTACCAATAGAGAAACACT 168
Qy	41 AapserthrhserllyallaserProsergcluaapTrnglnglunaaglysearMet 60
Db	189 GATTCACACCTCTTAAATCAGCCATCTGAGAGTACTCAGCAAGAAATGCAACATG 248
Qy	61 PheserleutlthrtTpaamllaapglvleuaapleuaenlaenlaenlergluaagla 80
Db	249 TTTCTCTCTATTCCTGGAAATATGATGATGATGATGATGATGATGATGATGATGAT 308
Qy	81 ArgglvallyaserTytleu 87
Db	309 CAGAGGAGTGTCTCTACTTA 329
RESULT 23	
LOCUS	BP219740 582 bp mRNA linear EST 15-SEP-2004
DEFINITION	BP219740 Sugano cDNA library, caudate nucleus Homo sapiens CDNA
ACCESSION	BP219740
VERSION	BP219740.1 GI:52092643
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Tanyata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE	Hominidae; Homo.
AUTHORS	1 (bases 1 to 582)
TITLE	Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
JOURNAL	Mitsuhama-Sugano,J., Nakai,K. and Sugano,S.
PIUMED	Sequence comparison of human and mouse genes reveals a homologous
COMMENT	block structure in the promoter regions
	Genome Res. 14 (9), 1711-1718 (2004)
	15342556

Pred. No.: 8,83e-47 Length: 582
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP275810 (1-582)

QY 1 MetGUARGAlaleuanserTyrPheGUProProValGUluserAlaGUlUArg 20
DB 158 ATGAAAGGGCTCTGAACCTTCACTTCAGAGCTCCGGTGAAGAGAGCGCTTGAAGCGC 217
QY 21 ArgProGUlUThrIleSerGUProPolyThrTyValAspLeuThrAsnGUlUThr 40
DB 218 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 277
QY 41 AspSerThrThrSerIleSerProSerGUlUAspThrGlnGlnGUlUAsnGlySerMet 60
DB 278 GATTCACCACTTCTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGGCAGCATG 337
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGUlUArg 80
DB 338 TTCTCTCATTAACCTGGAATATGATGATTGATCTTAAACAATCTGTCAAGAGGGCT 397
QY 81 ArgGlyValCysSerTyrLeu 87
DB 398 CGAGGGGTGTGTCTACTTA 418

RESULT 26

BP275810 582 bp mRNA linear EST 16-SEP-2004
BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone
LOCUS KDN04583, mRNA sequence.

ACCESSION BP275810
VERSION BP275810.1 GI:52189542
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL

PUBMED 15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source 1..582
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KDN04583"
/issue_type="kidney"
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ORIGIN

Alignment Scores:

Pred. No.: 8,83e-47 Length: 582
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP275810 (1-582)

QY 1 MetGUARGAlaleuanserTyrPheGUProProValGUluserAlaGUlUArg 20
DB 149 ATGAAAGGGCTCTGAACCTTCACTTCAGAGCTCCGGTGAAGAGAGCGCTTGAAGCGC 208
QY 21 ArgProGUlUThrIleSerGUProPolyThrTyValAspLeuThrAsnGUlUThr 40
DB 209 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 268
QY 41 AspSerThrThrSerIleSerProSerGUlUAspThrGlnGlnGUlUAsnGlySerMet 60
DB 269 GATTCACCACTTCTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGGCAGCATG 328
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGUlUArg 80
DB 329 TTCTCTCATTAACCTGGAATATGATGATTGATCTTAAACAATCTGTCAAGAGGGCT 388
QY 81 ArgGlyValCysSerTyrLeu 87
DB 389 CGAGGGGTGTGTCTACTTA 409

RESULT 27

BP195721 583 bp mRNA linear EST 14-SEP-2004
BP195721 Sugano cDNA library, brain Homo sapiens cDNA clone
LOCUS ADB08961, mRNA sequence.

ACCESSION BP195721
VERSION BP195721.1 GI:52039998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 583)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL

PUBMED 15342556
Contact: Yutaka Suzuki
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Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source 1..583
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADB08961"
/issue_type="brain"
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ORIGIN

Alignment Scores:

Pred. No.: 8,85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP195721 (1-583)

QY 1 MetGUARGAlaleuanserTyrPheGUProProValGUluserAlaGUlUArg 20
DB 217 ATGAAAGGGCTCTGAACCTTCACTTCAGAGCTCCGGTGAAGAGAGCGCTTGAAGCGC 276
QY 21 ArgProGUlUThrIleSerGUProPolyThrTyValAspLeuThrAsnGUlUThr 40
DB 277 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 336

QY 41 ApsSerThrThrSerIleSerProSerGluAapThrGlnGlnGluSerMet 60
|||||
DB 337 GATTTCACCACTTCTAAATCAAGCCATCTGAAGATACACAGAAATGCGACATG 396
QY 61 PheSerLeuIleThrTyrAsnIleAapGlyLeuAapLeuAsnAseSerGluArgAla 80
|||||
DB 397 TTCTCTCATTAACCTGGAATATTGATGATTAATCTTAAACAAATCTGCAGAGAGGCT 456
QY 81 ArgGlyValCysSerTyrLeu 87
|||||
DB 457 CGAGGGGTGTGTTCTACTTA 477
RESULT 28
LOCUS BP262103 583 bp mRNA linear EST 16-SEP-2004
DEFINITION BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HSI05902, mRNA sequence.
ACCESSION BP262103
VERSION BP262103.1 GI:52177334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 583)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSI05902"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"
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Alignment Scores:
Pred. No.: 8.85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP262103 (1-583)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
|||||
DB 94 ATGGAAGAGGCTCTGAACCTTCACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAGAGC 153
QY 21 ArgProGluThrIleSerGluProIyThrTyrValAapLeuThrAsnGluGluThrThr 40
|||||
DB 154 GCACTGAAACATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 213
QY 41 ApsSerThrThrSerIleSerProSerGluAapThrGlnGlnGluSerMet 60
|||||
DB 214 GATTTCACCACTTCTAAATCAAGCCATCTGAAGATACACAGAAATGCGACATG 273
QY 61 PheSerLeuIleThrTyrAsnIleAapGlyLeuAapLeuAsnAseSerGluArgAla 80
|||||
DB 274 TTCTCTCATTAACCTGGAATATTGATGATTAATCTTAAACAAATCTGCAGAGAGGCT 333

QY 81 ArgGlyValCysSerTyrLeu 87
|||||
DB 334 CGAGGGGTGTGTTCTACTTA 354
RESULT 29
LOCUS BP262741 583 bp mRNA linear EST 16-SEP-2004
DEFINITION BP262741 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HSI07919, mRNA sequence.
ACCESSION BP262741
VERSION BP262741.1 GI:52177972
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 583)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..583
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/mol_type="mRNA"
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/clone="HSI07919"
/tissue_type="small intestine"
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ORIGIN
Alignment Scores:
Pred. No.: 8.85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP262741 (1-583)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
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DB 30 ATGGAAGAGGCTCTGAACCTTCACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAGAGC 89
QY 21 ArgProGluThrIleSerGluProIyThrTyrValAapLeuThrAsnGluGluThrThr 40
|||||
DB 90 GCACTGAAACATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 149
QY 41 ApsSerThrThrSerIleSerProSerGluAapThrGlnGlnGluSerMet 60
|||||
DB 150 GATTTCACCACTTCTAAATCAAGCCATCTGAAGATACACAGAAATGCGACATG 209
QY 61 PheSerLeuIleThrTyrAsnIleAapGlyLeuAapLeuAsnAseSerGluArgAla 80
|||||
DB 210 TTCTCTCATTAACCTGGAATATTGATGATTAATCTTAAACAAATCTGCAGAGAGGCT 269
QY 81 ArgGlyValCysSerTyrLeu 87
|||||
DB 270 CGAGGGGTGTGTTCTACTTA 290
RESULT 30
LOCUS BP319548 583 bp mRNA linear EST 17-SEP-2004

DEFINITION BP19548 Sugano cDNA library, pericardium Homo sapiens cDNA clone
PCD11128, mRNA sequence.
ACCESSION BP19548
VERSION BP19548.1 GI:52248523
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,U., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PCD11128"
/issue_type="pericardium"
/clone_lib="Sugano cDNA library, pericardium"
ORIGIN
Alignment Scores:
Pred. No.: 8,856-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP19548 (1-583)
QY 1 MetGluAgaAlaLeuAunSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 209 ATGGAAGAGGCTGGAACCTCTCACTTCGAGCTCCGGTGGAGAGAGCCGCTTGGAAGCC 268
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 269 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACCT 328
QY 41 AapSerThrThrSerIleSerIleSerProSerGluAapThrGlnGlnGluAunGlySerMet 60
Db 329 GATTCACCACTTCTAATAATCAGCCACTGAAGATCTCAAGCAAGAAATGGCAGCAGT 388
QY 61 PheSerLeuIleThrTyrPheAsnIleAspGlyLeuAapLeuAunAunLeuSerGluArgAla 80
Db 389 TTCTCTCATTAACCTGGAATATTGATGATTGAATCTTAACCAATCTGTCAAGAGAGGCT 448
QY 81 ArgGlyValCysSerTyrLeu 87
Db 449 CGAGGGGTGTCTTCTTACTTA 469
RESULT 31
LOCUS BU783229 583 bp mRNA linear EST 11-OCT-2002
DEFINITION In01a08.v1 Human insulinoma Homo sapiens cDNA clone IMAGE:6123158
ACCESSION BU783229 5' similar to TM:095551 O95551 DJ0043.3 ;, mRNA sequence.
VERSION BU783229.1 GI:23827207
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Breestelli,J., Gradowh,G., Clifton,S.,
Hillier,L., Maria,M., Pape,D., Wylie,T., Martin,J., Bilestan,A.,
Schmitt,A., Treising,B., Ritter,E., Konko,I., Bennett,J.,
Williams,T., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: In01a08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gldco
High quality sequence atop: 430.
FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:6123158"
/issue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
(stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas Est project library."
ORIGIN
Alignment Scores:
Pred. No.: 8,856-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BU783229 (1-583)
QY 1 MetGluAgaAlaLeuAunSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 158 ATGGAAGAGGCTGGAACCTCTCACTTCGAGCTCCGGTGGAGAGAGCCGCTTGGAAGCC 217
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 218 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACCT 277
QY 41 AapSerThrThrSerIleSerIleSerProSerGluAapThrGlnGlnGluAunGlySerMet 60
Db 278 GATTCACCACTTCTAATAATCAGCCACTGAAGATCTCAAGCAAGAAATGGCAGCAGT 337
QY 61 PheSerLeuIleThrTyrPheAsnIleAspGlyLeuAapLeuAunAunLeuSerGluArgAla 80
Db 338 TTCTCTCATTAACCTGGAATATTGATGATTGAATCTTAACCAATCTGTCAAGAGAGGCT 397

QY 81 ArgGlyValCysSerTyrLeu 87
 DB 398 CGAGGGGTGTGTTCTACTTA 418

RESULT 32
 BP263059
 LOCUS BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA
 accession BP263059
 version BP263059.1 GI:52178290
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens

REFERENCE
 AUTHORS Suzuki Y., Yamashita R., Shiota M., Sakakibara Y., Chiba J.,
 Mizushima-Sugano J., Nakai K. and Sugano S.
 Title Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp

FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /tissue_type="small intestine"
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ORIGIN

Alignment Scores:
 Pred. No.: 8.87e-47 Length: 584
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP263059 (1-584)

QY 1 MetGluAgaAlaLeuAnsSerTyrRheGluProProValGluGluSerAlaLeuGluArg 20
 DB 83 ATGGAAGAGGCTCTGAACCTCTACTTCGAGCCTCCGTCGAGAGAGCCCTTGGAAACGC 142

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
 DB 143 CGACCTGAACCATCTCTGAGCCCAAGACCTAATGTTGACCTAACCAATGAAGAAACAACT 202

QY 41 AepSerThrThrSerIleSerProSerGluAepThrGlnGlnuAnGlySerMet 60
 DB 203 GATTCACACACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 262

QY 61 PheSerLeuIleThrThrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
 DB 263 TTCTCTCATTAACCTGGAATATGATGATTGAATCAACAACTGTGCAGAGAGGCT 322

QY 81 ArgGlyValCysSerTyrLeu 87
 DB 323 CGAGGGGTGTGTTCTACTTA 343

RESULT 33
 BP348623
 LOCUS BP348623 584 bp mRNA linear EST 17-SEP-2004

DEFINITION BP348623 Sugano cDNA library, brain Homo sapiens cDNA clone
 SZR01143, mRNA sequence.
 accession BP348623
 version BP348623.1 GI:52278608
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens

REFERENCE
 AUTHORS Suzuki Y., Yamashita R., Shiota M., Sakakibara Y., Chiba J.,
 Mizushima-Sugano J., Nakai K. and Sugano S.
 Title Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp

FEATURES
 source
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 /organism="Homo sapiens"
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 /clone="SZR01143"
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ORIGIN

Alignment Scores:
 Pred. No.: 8.87e-47 Length: 584
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP348623 (1-584)

QY 1 MetGluAgaAlaLeuAnsSerTyrRheGluProProValGluGluSerAlaLeuGluArg 20
 DB 190 ATGGAAGAGGCTCTGAACCTCTACTTCGAGCCTCCGTCGAGAGAGCCCTTGGAAACGC 249

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
 DB 250 CGACCTGAACCATCTCTGAGCCCAAGACCTAATGTTGACCTAACCAATGAAGAAACAACT 309

QY 41 AepSerThrThrSerIleSerProSerGluAepThrGlnGlnuAnGlySerMet 60
 DB 310 GATTCACACACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 369

QY 61 PheSerLeuIleThrThrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
 DB 370 TTCTCTCATTAACCTGGAATATGATGATTGAATCAACAACTGTGCAGAGAGGCT 429

QY 81 ArgGlyValCysSerTyrLeu 87
 DB 430 CGAGGGGTGTGTTCTACTTA 450

RESULT 34
 BP236074
 LOCUS BP236074 588 bp mRNA linear EST 15-SEP-2004
 DEFINITION BP236074 Sugano cDNA library, coronary artery endothelial cell Homo
 sapiens cDNA clone HCR06784, mRNA sequence.
 accession BP236074
 version BP236074.1 GI:52108984
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens

REFERENCE
 AUTHORS
 Title
 JOURNAL
 PUBMED
 COMMENT

REFERENCE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
AUTHORS Homiidae; Homo.
TITLE (bases 1 to 588)
JOURNAL Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
PUBMED Mitsuhashi-Sugano, J., Nakai, K. and Sugano, S.
COMMENT Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
1534256
CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
FEATURES
source
1..588
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR06784"
/issue_type="coronary artery"
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ORIGIN
Alignment Scores:
Pred. No.: 8.95e-47 Length: 588
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Gaps: 0
Indels: 0
DB: 3
US-10-757-745-2_COPY_54_140 (1-87) x BP236074 (1-588)
QY 1 MetGluArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 186 ATGGAAAGGGGCTCGAACTCTCACTTCGAGCTCCGGTGGAGAGAGCCGCTTGGAAAGC 255
QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThr 40
Db 256 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAGAAACAAC 315
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGluGluGluGluSerMet 60
Db 316 GATTCACCACTTCTTAAATCAAGCCCATCTGAGATCTCGACAAAGAAATGGCAGCANTG 375
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 376 TTCTCTCATTAACCTGGAATATTGATGATTGATTAATCAATCTGTCTGAGAGGGCT 435
QY 81 ArgGlyValCysSerTyLeu 87
Db 436 CGAGGGGTGTGTTCTTACTTA 456
RESULT 35
AL703449 602 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZP686G0621.r1.686 (synonym: hicc3) Homo sapiens cDNA clone
DEFINITION DKFZP686G0621.5', mRNA sequence.
ACCESSION AL703449
VERSION AL703449.1 GI:19668804
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 602)
AUTHORS Anorgey, W., Wirtner, U., Mewes, W., Weill, B. and Wiemann, S.
TITLE EST (Anorgey, W., Wirtner, U., Mewes, W., Weill, B. and Wiemann, S.)
JOURNAL Unpublished (1999)

COMMENT Contact: MIPS
MIPS
Institute of Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de/
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZP686G0621) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
FEATURES
source
1..602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686G0621"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hicc3)"
/note="Vector: pT7D1Ex2; Site_1: SflTA; Site_2: SflTB,
cDNA-collection"
ORIGIN
Alignment Scores:
Pred. No.: 9.23e-47 Length: 602
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Gaps: 0
Indels: 0
DB: 1
US-10-757-745-2_COPY_54_140 (1-87) x AL703449 (1-602)
QY 1 MetGluArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 161 ATGGAAAGGGGCTCGAACTCTCACTTCGAGCTCCGGTGGAGAGAGCCGCTTGGAAAGC 220
QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThr 40
Db 221 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAGAAACAAC 280
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGluGluGluGluSerMet 60
Db 281 GATTCACCACTTCTTAAATCAAGCCCATCTGAGATCTCGACAAAGAAATGGCAGCANTG 340
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 341 TTCTCTCATTAACCTGGAATATTGATGATTGATTAATCAATCTGTCTGAGAGGGCT 400
QY 81 ArgGlyValCysSerTyLeu 87
Db 401 CGAGGGGTGTGTTCTTACTTA 421
RESULT 36
CB069952 621 bp mRNA linear EST 21-JAN-2003
LOCUS CB069952
DEFINITION is1610.y1 HR65 islet Homo sapiens cDNA clone IMAGE:6554035 5'
similar to TR:095551.095551.DJ30M3.3', mRNA sequence.
ACCESSION CB069952
VERSION CB069952.1 GI:27814472
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Mellon, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Pearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blakesh, A.,

Schmitt, A., Theising, B., Rafter, E., Ronko, I., Bennett, J.,
Caretens, M., Gibbons, M., McCann, R., Cole, R., Teagataienhvi, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 1631610.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bionh.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 476.
Location/Qualifiers

FEATURES

1..621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5534035"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Alignment Scores:
Pred. No.: 9,616-47 Length: 621
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x CB069952 (1-621)

OY 1 MetGUUAGUAlaLeuAsnSerTyrrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 166 ATGGAAAGGGCTCTGAACCTCTACCTCGAGCTCCGCTGAGAGAGCCCTTGGAAACC 225
OY 21 ArgProGluThrIleSerGluProIysThrTyrrValAspLeuThrAsnGluGluThr 40
DB 226 CCACTGAAACCACTCTGAGCCCAAGACCTTAAGTTGACCTTAACCAATGAAGAAACAAC 285
OY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 286 GATTCCACCACTCTTAATATCAGCCCATCTGAAGATACACAGCAAGAAAATGGCAGCAG 345
OY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 346 TTCTCTCATTAACCTGGAATATTGATGATTAGATTAAACATCTGTCAAGAGGGCT 405
OY 81 ArgGlyValCysSerTyrLeu 87
DB 406 CAGGGGGTGTCTCTACTTA 426
RESULT 37
CB157906 634 bp mRNA linear EST 29-JAN-2003
LOCUS

DEFINITION K-EST0217150 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-5-F06
5', mRNA sequence.
ACCESSION CB157906
VERSION CB157906.1 GI:28143040
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 634)
REFERENCE Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: F column: 0634.
High quality sequence stop: 634.
Location/Qualifiers

FEATURES

1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L18POOL1n1-5-F06"
/cell_line="SN-354+Cho-CK+Cho-CK+HLK-3"
/lab_host="Top10P"
/clone_lib="L18POOL1n1"
/note="Organ: Liver; Vector: pRTT3-Pac; Site 1: EcoRI;
Site 2: NotI; The library was constructed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lemmon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Alignment Scores:
Pred. No.: 9,886-47 Length: 634
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x CB157906 (1-634)

OY 1 MetGUUAGUAlaLeuAsnSerTyrrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 112 ATGGAAAGGGCTCTTAACCTCTACTTCAGCTCCGCTGAGAGAGCCCTTGGAAACC 171
OY 21 ArgProGluThrIleSerGluProIysThrTyrrValAspLeuThrAsnGluGluThr 40
DB 172 CCACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 231
OY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 232 GATTCCACCACTCTTAATATCAGCCCATCTGAAGTACTCAGCAAGAAAATGGCAGCAG 291
OY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 292 TTCTCTCATTAACCTGGAATATTGATGATTAGATTAAACATCTGTCAAGAGGGCT 351
OY 81 ArgGlyValCysSerTyrLeu 87
DB 352 CAGGGGGTGTCTCTACTTA 372
RESULT 38
CB157906 634 bp mRNA linear EST 29-JAN-2003
LOCUS

CV023369
LOCUS 634 bp mRNA linear EST 20-AUG-2004
DEFINITION 288 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC017553, mRNA sequence.
ACCESSION CV023369
VERSION CV023369.1 GI:51481130
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 634)
REFERENCE Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
Vandenhaute,J., Quack,M.E., Albala,J.S., Hill,D.E. and Vidal,M.,
Human ORFome Version 1.1: a platform for Reverse Proteomics
Genome Res. (2004) in press
CONTACT: Vidal M
TITLE Marc Vidal Laboratory
JOURNAL Dana Farber Cancer Institute
COMMENT 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers
FORWARD: ATGAGTGGGAGGAGTTCCTGCA
BACKWARD: TACATATTATATCTAGTGCACAGAG
Insert Length: 634 Std Error: 32.00
Plate: 11008 row: 05 column: F
Seq primer: ACTGCGCGTCTTTTACACGTCGTGACTGGGAAAAC
High quality sequence start: 97
High quality sequence stop: 633
POLYA-No.
FEATURES
location/Qualifiers
source 1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cbase_type="mixed"
/clone_id="Full Length cDNA from the Mammalian Gene
Collection"
/note="Vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor Vector. Reference: MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"

ALIGNMENT SCORES:
Pred. No.: 9.88e-47 Length: 634
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CV023369 (1-634)

QY 1 MetGUAAGAlaLeuAnSerTyrPheGluProProValAGluGluSerAlaLeuGUAArg 20
DB 160 ATGGAAGGGGCTCTGAACCTCTCTGAGCTCCGGTGGAGAGAGCCCTTGAAGCC 219

QY 21 ArgProGluThrIleSerGluProGlyThrTyrValaAspLeuThrAsnGluGluThrThr 40
DB 220 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTTAACAATGAAGAAACAAC 279

QY 41 AspSerThrThrseryleIleSerProSerGluAspThrGluGluAsnGlySerMet 60
DB 280 GATTCACACCACTTCTAAATAGCCCATCTGAGAGATCTCACAGAAAGAAATGCAAGCATG 339

QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 340 TTCTCTCTCATTCAGGATTTGATGATGATTCATAACATCTCTCAGAGAGGCT 339

QY 81 ArgGlyValCysSerTyrIleu 87
DB 400 CGAGGGGTGTGTTCTACTTA 420

RESULT 39
B133830 644 bp mRNA linear EST 30-JUN-2001
LOCUS 602999339P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141577 5',
mRNA sequence.
DEFINITION B133830.1 GI:15018487
ACCESSION B133830
VERSION B133830.1 GI:15018487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 644)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
<http://image.jml.gov>
Plate: L14M11348 row: n column: 10
High quality sequence stop: 531.
location/Qualifiers
source 1..644
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5141577"
/cbase_type="cervical carcinoma cell line"
/lab_name="MDA108"
/clone_id="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6, Site 1: NotI,
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 Kb. Library prepared by Life
Technologies."

ALIGNMENT SCORES:
Pred. No.: 1.01e-46 Length: 644
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x B133830 (1-644)

QY 1 MetGUAAGAlaLeuAnSerTyrPheGluProProValAGluGluSerAlaLeuGUAArg 20
DB 147 ATGGAAGGGGCTCTGAACCTCTCTGAGCTCCGGTGGAGAGAGCCCTTGAAGCC 206

QY 21 ArgProGluThrIleSerGluProGlyThrTyrValaAspLeuThrAsnGluGluThrThr 40
DB 207 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTTAACAATGAAGAAACAAC 266

QY 41 AspSerThrThrSerValIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 267 GATTCACACACTTCTAAATATCAGCCATCTGAAGATCTACAGCAAGAAATATGCGACATG 326
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 327 TTCTCTCATTAACCTGGAATATGATGATTAATGATCTAAACAATCTGTCAAGAGGGCT 386
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 387 CGAGGGGTGTGTCTCTACTTA 407

RESULT 40

LOCUS CR753214 652 bp mRNA linear EST 01-SEP-2004
 DEFINITION DKFZp4691195.1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
 CR753214
 ACCESSION CR753214 GI:51845629
 VERSION EST
 KEYWORDS

SOURCE

ORGANISM Pongo pygmaeus (orangutan)
 Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Pongo.
 1 (bases 1 to 652)
 Ansoerge, W., Krieger, S., Regiert, T., Ritzmuller, C., Schwager, B.,
 Mewes, H.W., Weil, B., Amd, C., Osanger, A., Fobo, G., Han, M. and
 Wiemann, S.
 Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 Unpublished (2004)
 CONTACT: MIPS

TITLE

JOURNAL Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 COMMENT Unpublished (2004)

FEATURES

source

1..652
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp4691195"
 /tissue_type="kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_idb="469 (synonym: pkid1)"
 /note="Vector: pSport1_Sci, Site_1: SfilA, Site_2: SfilB"
 Location/Qualifiers
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp4691195
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-46 Length: 652
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR753214 (1-652)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 177 ATGGAAGAGGCTCTGAATCTTCACTTCGAGCTCCGGTGAAGAGGCGCTTGGAGCGC 236
 QY 21 ArgProGluThrIleSerGluProLysTyrTyrValAspLeuThrAsnGluGluThrThr 40
 DB 237 CGCCCTGAACCATCTCTGAGCCCAAGACCTAATGTTGACCTAACCAATGAAGAAACAACCT 296

QY 41 AspSerThrThrSerValIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 267 GATTCACACACTTCTAAATATCAGCCATCTGAAGATCTACAGCAAGAAATATGCGACATG 356
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 357 TTCTCTCATTAACCTGGAATATGATGATTAATGATCTAAACAATCTGTCAAGAGGGCT 416
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 417 CGAGGGGTGTGTCTCTACTTA 437

RESULT 41

LOCUS CN298920 657 bp mRNA linear EST 16-MAY-2004
 DEFINITION U7000600170525 GRN PRENEU Homo sapiens cDNA 5', mRNA sequence.
 CN298920
 ACCESSION CN298920.1 GI:47315334
 VERSION EST
 KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 657)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.
 Transcriptionome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 15146197
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 657 Std Error: 0.00.

TITLE

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT PUBLISHED 15146197

FEATURES

source

1..657
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_idb="GRN PRENEU"
 /note="Oligo dT primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic acid and mitogens."

ORIGIN

Alignment Scores:

Pred. No.: 1.03e-46 Length: 657
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CN298920 (1-657)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 116 ATGGAAGAGGCTCTGAATCTTCACTTCGAGCTCCGGTGAAGAGGCGCTTGGAGCGC 175
 QY 21 ArgProGluThrIleSerGluProLysTyrTyrValAspLeuThrAsnGluGluThrThr 40
 DB 176 CGACCTGAACCATCTCTGAGCCCAAGACCTAATGTTGACCTAACCAATGAAGAAACAACCT 235
 QY 41 AspSerThrThrSerValIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

Db 236 GATTCCACACCTTCTAAATCAGCCCATCTAAGATCTCAGCAAGAAATGCGACATG 295
 Qy 61 PheserleuileThrTTPAsnileAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
 Db 296 TTCTCTCATTAACCTCGAATATGATGATTGATCTAAACAATCTGTCAAGAGGCT 355
 Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 356 CGAGGGGTGTCTTCTACTTA 376

RESULT 42
 BG719113
 LOCUS 60269045F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831186 5',
 DEFINITION mRNA sequence.
 ACCESSION BG719113
 VERSION BG719113.1 GI:13998300
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 678)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsbs-remail.nih.gov
 Tissue Procurement: Miklos Palkevics, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L14M10753 row: 1 column: 11
 High quality sequence stop: 672.
 Location/Qualifiers

FEATURES

Source

1..678
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4831186"
 /lab_host="DH10B"
 /clone_1lb="NIH_MGC_97"
 /note="Organ: testis; Vector: pBluescriptPR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 (GTCGAG); Oligo-dT primed using primer
 5'-TTTTTTTTTTTNN-3', size-selected for average
 insert size 2.2 kb and normalized to R0F 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI). National Institutes of Health. Note: this is
 a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1,086-46 Length: 678
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG719113 (1-678)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 Db 182 ATGGAAAGGCGCTCTGAACTCTGAGCTCCGATGGAGAGAGCGCTTGAGAGCG 241

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
 Db 242 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCTTAACAAAGAAACAACACT 301
 Qy 41 AspSerThrThrSerLeuIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 Db 302 GATTCCACACCTTCTAAATCAGCCCATCTGGAAGATACACAGAAAGAAATGCGACATG 361
 Qy 61 PheserleuileThrTTPAsnileAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
 Db 362 TTCTCTCATTAACCTCGAATATGATGATTGATCTAACAATCTGTCAAGAGGCT 421
 Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 422 CGAGGGGTGTCTTCTACTTA 442

RESULT 43
 CR767236
 LOCUS 701 bp mRNA linear EST 23-SEP-2004
 DEFINITION DKFZ469E1236_r1 469 (synonym: PKid1) Pongo pygmaeus cDNA clone
 DKFZ469E1236 5', mRNA sequence.
 ACCESSION CR767236
 VERSION CR767236.1 GI:52609173
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Pongo.
 1 (bases 1 to 701)
 Ansoerge, W., Krieger, S., Regiert, T., Rittmeyer, C., Schwager, B.,
 Mewes, H.W., Well, B., Amdt, C., Oeinger, A., Fobo, G., Han, M. and
 Wiemann, S.
 Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 Unpublished (2004)
 COMMENT Contact: MIPS

TITLE MIPS
 JOURNAL
 AUTHORS
 REFERENCE
 Ingolstaedter Landert, I., D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; rlln, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZ469E1236
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
 Location/Qualifiers

FEATURES

Source

1..701
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZ469E1236"
 /cissue="DKFZ469E1236"
 /cissue="Kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="469 (synonym: PKid1)"
 /note="Vector: pSport1_Sfi1; Site_1: Sfi1a; Site_2: Sfi1b"

ORIGIN

Alignment Scores:
 Pred. No.: 1,136-46 Length: 701
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR767236 (1-701)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 Db 88 ATGGAAAGGCGCTCTGAACTCTGAGCTCCGATGGAGAGAGCGCTTGAGAGCG 147

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us-10-757-745-2_copy_54_140.txt

Page 30

/clone_11b="GRN PREHEP"
/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:

Pred. No.:	1,156-46	Length:	711
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CN298923 (1-711)

QY 1 MetGUARGAlaLeuaAnSerTyPheGluPProPValGluGluSerAlaLeuGluArg 20
Db 125 ATGGAAGGGCTCTGAATCTTCTGAGCTCCGGTGAAGAGAGCGCTTGAGACGC 184
QY 21 ArgProGluThrIleSerGluProIleThrTyValAspLeuThrAsnGluGluThr 40
Db 185 CGACCTGAACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 244
QY 41 AapSerThrThrSerIleSerProSerGluAapThrGlnGlnGluAsnGlySerMet 60
Db 245 GATTCACACCTCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 304
QY 61 PheSerLeuIleThrTTPAenlleaPglyLeuaPleuaAnleuSerGluArgAla 80
Db 305 TTCTCTCTCATTAACCGAATATTGATGATTAAGATCTTAACCAATCTGTCAAGAGGGCT 364
QY 81 ArgGlyValCysSerTyLeu 87
Db 365 CGAGGGGTGTGTTCTTACTTA 385

RESULT 46
LOCUS CN298922 729 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600077717 GRN_PHEHP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN298922
VERSION CN298922.1 GI:47315336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 729)
TITLE Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lobkowsky, J. and Stanton, L.W.
JOURNAL Transcriptional characterization elucidates signaling networks that
control human ES cell growth and differentiation
PUBMED Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/db_xref="taxon:9606"
/feature_type="embryonic stem cells, cell lines H1, H7, and H9"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p22), H7 (p23),
and H9 (p26) maintained in feeder-free conditions"

FEATURES

source
1..729
/organism="Homo sapiens"
/db_xref="taxon:9606"
/feature_type="embryonic stem cells, cell lines H1, H7, and H9"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p22), H7 (p23),
and H9 (p26) maintained in feeder-free conditions"

from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:

Pred. No.:	1,156-46	Length:	729
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CN298922 (1-729)

QY 1 MetGUARGAlaLeuaAnSerTyPheGluPProPValGluGluSerAlaLeuGluArg 20
Db 152 ATGGAAGGGCTCTGAATCTTCTGAGCTCCGGTGAAGAGAGCGCTTGAGACGC 211
QY 21 ArgProGluThrIleSerGluProIleThrTyValAspLeuThrAsnGluGluThr 40
Db 212 CGACCTGAACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 271
QY 41 AapSerThrThrSerIleSerProSerGluAapThrGlnGlnGluAsnGlySerMet 60
Db 272 GATTCACACCTCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 331
QY 61 PheSerLeuIleThrTTPAenlleaPglyLeuaPleuaAnleuSerGluArgAla 80
Db 332 TTCTCTCTCATTAACCGAATATTGATGATTAAGATCTTAACCAATCTGTCAAGAGGGCT 391
QY 81 ArgGlyValCysSerTyLeu 87
Db 392 CGAGGGGTGTGTTCTTACTTA 412

RESULT 47
LOCUS CN298924 729 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424496911 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN298924
VERSION CN298924.1 GI:47315338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 729)
TITLE Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lobkowsky, J. and Stanton, L.W.
JOURNAL Transcriptional characterization elucidates signaling networks that
control human ES cell growth and differentiation
PUBMED Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/db_xref="taxon:9606"
/feature_type="embryonic stem cells, cell lines H1, H7, and H9"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p22), H7 (p23),
and H9 (p26) maintained in feeder-free conditions"

FEATURES

source
1..729
/organism="Homo sapiens"
/db_xref="taxon:9606"
/feature_type="embryonic stem cells, cell lines H1, H7, and H9"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p22), H7 (p23),
and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Alignment Scores:

Alignment Scores:	1.19e-46	Length:	729
Pred. No.:	448.00	Matches:	87
Score:	100.0%	Conservative:	0
Percent Similarity:	100.0%	Mismatches:	0
Best Local Similarity:	100.0%	Indels:	0
Query Match:	100.0%	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CN298924 (1-729)

QY 1 MetGUARGAlaLeuanserTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db ATGAAAGGGGCTTGAAGCTCTGAGCCCTCGGAGAGAGAGCCCTTGAGAGCC 153
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db CGACCTGAACCATCTCTGAGCCCAAGACCTAAGTGAACCTAAGCAATGAAGAAACACT 213
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db GATTCACACCACTTCAAAATGAGCCCATCTGAAGATACACAGCAAGAAATGCGACGATG 273
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db TTCTCTCATTAACCTGGAATGATGATGATTAACATCTGTGAGAGAGGCT 333
QY 81 ArgGlyValCysSerTyrLeu 87
Db 334 CGAGGGGTGTGTTCTACTTA 354

RESULT 48

CX760857

LOCUS

CX760857 731 bp mRNA linear EST 24-JAN-2005

AGENCOURT 40963383 NIH MGC 281 Homo sapiens cDNA clone

ACCESSION

CX760857

VERSION

CX760857.1 GI:58057513

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Hemo 1 to 731)

1 (bases 1 to 731)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics / NIH

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Meit Firoo

cDNA Library Preparation: Express Genomics

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov/

Plate: LLM15944 row: b column: 14

High quality sequence atop: 574.

Location/Qualifiers

1..731

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:7783600"

/tissue_type="pluripotent cell line derived from

blastocyst inner cell mass"

/lab_host="DH10B Tona"

/clone_id="NIH_MGC_281"

ORIGIN

Alignment Scores:

Alignment Scores:	1.19e-46	Length:	731
Pred. No.:	448.00	Matches:	87
Score:	100.0%	Conservative:	0
Percent Similarity:	100.0%	Mismatches:	0
Best Local Similarity:	100.0%	Indels:	0
Query Match:	100.0%	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CX760857 (1-731)

QY 1 MetGUARGAlaLeuanserTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db ATGAAAGGGGCTTGAAGCTCTGAGCCCTCGGAGAGAGAGCCCTTGAGAGCC 223
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db CGACCTGAACCATCTCTGAGCCCAAGACCTAAGTGAACCTAAGCAATGAAGAAACACT 283
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db GATTCACACCACTTCAAAATGAGCCCATCTGAAGATACACAGCAAGAAATGCGACGATG 343
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db TTCTCTCATTAACCTGGAATGATGATGATTAACATCTGTGAGAGAGGCT 403
QY 81 ArgGlyValCysSerTyrLeu 87
Db 404 CGAGGGGTGTGTTCTACTTA 424

RESULT 49

B1258848

LOCUS

B1258848 767 bp mRNA linear EST 17-JUL-2001

60296633P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109303 5',

mRNA sequence.

B1258848

B1258848.1 GI:14815606

EST.

SOURCE

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Hemo. 1 (bases 1 to 767)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Office of Cancer Genomics, Inc.

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov/

/note="Organ: Blastocyst; Vector: pExpress-1; Site: 1; ScoreV; Site 2: NotI; RNA obtained from pluripotent cell line derived from blastocyst inner cell mass (cell line HSF-6, NIH Registry designation UC06. Positive for OCT4 expression by rtPCR, positive for SSEA-3, SSEA-4, Tra-1-81, Tra-1-60 by immunofluorescence. Negative for SSEA-1 by immunofluorescence passage 62. cDNA was primed using oligo-dT primer: 5'-pGACTAGTCTAGATCGGAGCGCCGCC(17)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 2.0 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_280) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.rst

Page 32

Plate: L1AM11264 row: m column: 16
High quality sequence stop: 758.
Location/Qualifiers

FEATURES

source
1..767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5109303"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_idb="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; Nci; Site 2: Salt; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 1.27e-46 Length: 767
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 2
US-10-757-745-2_COPY_54_140 (1-87) x B1258848 (1-767)

OY 1 MetG1AAGAlaleuAnserTyPheG1uPProProVa1G1uG1uSerAlaleuG1uArg 20
DB 97 ATGGAAGGGCTCTGAACCTCTGAGCTCCGATGAGAGAGAGCGCTTGGAACGC 156
OY 21 ArgProG1uThri1seGc1uProlyeThrTyValAspleuThrasnG1uG1uThrThr 40
DB 157 CGACCTGAACCATCTCTGAGCCCAAGCCTATGACCTAAACCAATGAAGAAACAAC 216
OY 41 AspSerThrTherSerTy1seerProserG1uAspThrG1ng1uAnG1ySerMet 60
DB 217 GATTCACACACTCTTAATATCAGCCCATCTGAATATCTCAGAAAGAAATGCGAGCGCT 276
OY 61 PheSerLeu1leThrTyPasn1leAspG1yLeuAspleuAnsnleuSerG1uArgAla 80
DB 277 TTCCTCTCATTAACCTGAATATGATGATTAATCAACAATCTGTCAAGAGGCGCT 336
OY 81 ArgG1yValCyseerTyLeu 87
DB 337 CGAGGGGTGTCTCTACTTA 357

RESULT 50
B1754101 774 bp mRNA linear EST 25-SEP-2001
LOCUS 603027659P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197838 5',
DEFINITION mRNA sequence.
ACCESSION B1754101
VERSION B1754101.1 GI:15745679
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 774)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Invitrogen, Inc.
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Plate: L1AM11495 row: f column: 15
High quality sequence stop: 756.
Location/Qualifiers

FEATURES

source
1..774
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5197838"
/lab_host="DH10B"
/clone_idb="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; Nci; Site 2: B20KV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dt primed and directionally cloned. (B20KV site is destroyed upon cloning). Average insert size 1.5 kb. Insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 1.28e-46 Length: 774
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 3
US-10-757-745-2_COPY_54_140 (1-87) x B1754101 (1-774)

OY 1 MetG1AAGAlaleuAnserTyPheG1uPProProVa1G1uG1uSerAlaleuG1uArg 20
DB 219 ATGGAAGGGCTCTGAACCTCTGAGCTCCGATGAGAGAGAGCGCTTGGAACGC 278
OY 21 ArgProG1uThri1seGc1uProlyeThrTyValAspleuThrasnG1uG1uThrThr 40
DB 279 CGACCTGAACCATCTCTGAGCCCAAGCCTATGACCTAAACCAATGAAGAAACAAC 338
OY 41 AspSerThrTherSerTy1seerProserG1uAspThrG1ng1uAnG1ySerMet 60
DB 339 GATTCACACACTCTTAATATCAGCCCATCTGAATATCTCAGAAAGAAATGCGAGCGCT 398
OY 61 PheSerLeu1leThrTyPasn1leAspG1yLeuAspleuAnsnleuSerG1uArgAla 80
DB 399 TTCCTCTCATTAACCTGAATATGATGATTAATCAACAATCTGTCAAGAGGCGCT 458
OY 81 ArgG1yValCyseerTyLeu 87
DB 459 CGAGGGGTGTCTCTACTTA 479

RESULT 51
B6719977 786 bp mRNA linear EST 08-MAY-2001
LOCUS 602691335P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823452 5',
DEFINITION mRNA sequence.
ACCESSION B6719977
VERSION B6719977.1 GI:13999164
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 786)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Miklos Palcovite, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shizaki
Tohiyuki and Piero Carninci (RIKEN)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: InCyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 plate: LLM10733 row: f column: 09
 High quality sequence stop: 784.
 Location/Qualifiers

FEATURES

source

1..786
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4823432"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_97"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 (gtcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.2 kb and normalized to R0T 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1,31e-46 Length: 786
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG719977 (1-786)

OY 1 MetGluAAGAlaLeuAnserTyRphGluProProValGluGluSerAlaLeuGluArg 20
 DB 305 ATGGAAGAGGCTCTGAACCTCTCACTCGAGCCCTCGTGAAGAGAGCCCTTGGAACCC 364
 OY 21 ArgProGluThrIleSerGluProLyThrTyValAspLeuThrAsnGluGluThr 40
 DB 365 CGACCTGAACCATCTCTGAGCCCAAGACCTATGCTGACCTAACAATGAAGAAACAAT 424
 OY 41 AppSerThrTherSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 425 GATTCACCACTTCTAAATCAAGCCCATCTGAAGATACACAGCAAGAAATGACACATG 484
 OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 485 TTCTCTCTCATTAACCTGAACCATTTGATGATTAAGATCTAAACAATCTGTCAAGAGGCT 544
 OY 81 ArgGlyValCysSerTyLeu 87
 DB 545 CGAGGGGTGTCTCTACTTA 565

RESULT 52
 CX756424 799 bp mRNA linear EST 24-JAN-2005
 LOCUS AGENCOURT 41337854 NIH_MGC_281 Homo sapiens CDNA clone
 DEFINITION IMAGE:7779791 3', mRNA sequence.
 ACCESSION CX756424
 VERSION CX756424.1 GI:58053080
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 799)
 REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE

JOURNAL

Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Meri Firpo

COMMENT

CDNA Library Preparation: Express Genomics
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 plate: LLM15934 row: c column: 21
 High quality sequence stop: 579.
 Location/Qualifiers

FEATURES

source

1..799
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:7779791"
 /tissue_type="Pluripotent cell line derived from
 blastocyst inner cell mass"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_281"
 /note="Organ: Blastocyst; Vector: pExpress-1; Site 1:
 EcoRV; Site 2: NotI; RNA obtained from pluripotent cell
 line derived from blastocyst inner cell mass (cell line
 HSF-6, NIH Registry designation UC06. Positive for OCT4
 expression by rtPCR, positive for SSEA-3, SSEA-4,
 Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
 SSEA-1 by immunofluorescence Passage 62. CDNA was primed
 using oligo-dT primer:
 5'-pGACATGTTCTAGATCGGAGCGCCGCTT(25-3' and cloned into
 the pGCRV/NotI sites of pExpress-1. Size-selection >1.25
 kb resulted in an average insert size of 2.0 kb. This
 primary library is normalized (non-normalized by Express
 library is NIH_MGC_280) and was constructed by Express
 Genomics (Frederick, MD). Note: this is a Mammalian Gene
 Collection library."

ORIGIN

Alignment Scores:

Pred. No.: 1,34e-46 Length: 799
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CX756424 (1-799)

OY 1 MetGluAAGAlaLeuAnserTyRphGluProProValGluGluSerAlaLeuGluArg 20
 DB 177 ATGGAAGAGGCTCTGAACCTCTCACTCGAGCCCTCGTGAAGAGAGCCCTTGGAACCC 236
 OY 21 ArgProGluThrIleSerGluProLyThrTyValAspLeuThrAsnGluGluThr 40
 DB 237 CGACCTGAACCATCTCTGAGCCCAAGACCTATGCTGACCTAACAATGAAGAAACAAT 296
 OY 41 AppSerThrTherSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 297 GATTCACCACTTCTAAATCAAGCCCATCTGAAGATACACAGCAAGAAATGACACATG 356
 OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 357 TTCTCTCTCATTAACCTGAACCATTTGATGATTAAGATCTAAACAATCTGTCAAGAGGCT 416
 OY 81 ArgGlyValCysSerTyLeu 87
 DB 417 CGAGGGGTGTCTCTACTTA 437

RESULT 53

CX166335
LOCUS 810 bp mRNA linear EST 23-DEC-2004
DEFINITION HSEC2.39 B09.G1.A035 NIH_MGC_258 Homo sapiens cDNA clone
IMAGE:7469923.5, mRNA sequence.
ACCESSION CX166335
VERSION CX166335.1 GI:56796415
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 810)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Daniela S. Gerhard, Ph.D.
JOURNAL Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
COMMENT Email: cga@bbs-remail.nih.gov
Tissue Procurement: BresaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNLN),
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LHAM15771 row: d column: 17
Seq primer: JENREV (CAGGAACGCTATGACC)
High quality sequence stop: 810.
Location/Qualifiers
1..810
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7469923"
/sex="male"
/tissue_type="human embryonic stem cells differentiated to
an early endodermal cell type"
/cell_line="human embryonic stem cells"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_idb="NIH_MGC_258"
/note="Vector: pEXpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is BG01. Negative for AFP
expression. Passage number 40. cDNA primed using oligo-dT
primer: 5'-DCACTAGTTCAGATCGCGCGCGCCGCC(T)25-3' and
cloned into the EcoRV/NotI sites of pEXpress-1. This
primary library is non-normalized (normalized primary
library is NIH_MGC_259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."

ORIGIN
Alignment Scores:
Pred. No.: 1,36e-46 Length: 810
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
US-10-757-745-2_copy_54_140 (1-87) x CX166335 (1-810)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 117 ATGGAAGAGGGCTCTAACCCTCTACTTGTGACCCCTCGGTGAGAGAGCGCTTGAAAGCG 176
QY 21 ArgProGluThrIleSerGluProProLeuThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 177 CGACCTGAAACCATCTCTGAGCCCGAGACCTATGTTGACCTTAACCAATGAAAGAAACAAC 236
QY 41 AspSerThrThrSerIleIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 237 GATTCCACCACTTCTTAATATCATGATGATGATGATGATGATGATGATGATGATGATGATG 296
QY 61 PheSerLeuIleThrTyrPasnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 297 TTCTCTCTCATTAACCTGGAATATTTGATGATGATGATGATGATGATGATGATGATGATG 356
QY 81 ArgGlyValCysSerTyrLeu 87
DB 357 CGAGGGGTGTGTTCTTACTTA 377
RESULT 54
BI908925
LOCUS 838 bp mRNA linear EST 16-OCT-2001
DEFINITION 603067028F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215926.5',
mRNA sequence.
ACCESSION BI908925
VERSION BI908925.1 GI:16172029
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 838)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNLN)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LHAM1542 row: h column: 07
High quality sequence stop: 773.
Location/Qualifiers
1..838
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5215926"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_idb="NIH_MGC_118"
/note="Vector: pGV-SORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1,42e-46 Length: 838
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x B1908925 (1-838)

QY 1 MetGUARGAlaleuanserTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 161 ATGAAAGGGCTCTGAACCTCTTACCTTCGAGCTCCGGTGGAGAGAGCCCTTGGAGCC 220
QY 21 ArgProGluThrIleSerGluProLyThrTyrValAspLeuThrAsnGluGluThr 40
DB 221 CGACCTGAAGACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACA 280
QY 41 AspSerThrThrSerLyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 281 GATTCACACCACTCTCAAAATCAAGCCCATCTGAGAACTACAGCAAGAAATGCGCAG 340
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 341 TTCTCTCATTAACCTGGAATTTGATGATTTAGATCTAAACAACTGTCAAGAGGGCT 400
QY 81 ArgGlyValCysSerTyrLeu 87
DB 401 CGAGGGGTGTGTTCTACTTA 421

RESULT 55

CR765451

LOCUS CR765451 846 bp mRNA linear EST 23-SEP-2004
DEFINITION DKFZP469E2434.r1.469 (synonym: pkid1) Pongo pygmaeus cDNA clone
ACCESSION CR765451
VERSION CR765451
KEYWORDS CR765451.1 GI:52605526
EST.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pongo

1 (bases 1 to 846)

Ottenwelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A.,
Mewes, H.W., Weill, B., Amd, C., Osanger, A., Fobo, G., Han, M. and
Wieman, S.

Pongo pygmaeus mRNA (Ottenwelder, B., Obermaier, B.,
Deutschenbaur, S., et al.)

Unpublished (2004)

CONTACT: MIPS

COMMENT

TITLE

JOURNAL

COMMENT

COMMENT

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COMMENT

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FEATURES

source

1. 846
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP469E2434"
/issue_type="Kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Alignment Scores:

Pred. No.: 1.44e-46 Length: 846

Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR765451 (1-846)

QY 1 MetGUARGAlaleuanserTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 63 ATGAAAGGGCTCTGAACCTCTTACCTTCGAGCTCCGGTGGAGAGAGCCCTTGGAGCC 122
QY 21 ArgProGluThrIleSerGluProLyThrTyrValAspLeuThrAsnGluGluThr 40
DB 123 CGCCCTGAAGACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACA 182
QY 41 AspSerThrThrSerLyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 183 GATTCACACCACTCTCAAAATCAAGCCCATCTGAGAACTACAGCAAGAAATGCGCAG 242
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 243 TTCTCTCATTAACCTGGAATTTGATGATTTAGATCTAAACAACTGTCAAGAGGGCT 302
QY 81 ArgGlyValCysSerTyrLeu 87
DB 303 CGAGGGGTGTGTTCTACTTA 323

RESULT 56

BE784416

LOCUS BE784416 853 bp mRNA linear EST 20-OCT-2000
DEFINITION 601473891P1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876862 5',
ACCESSION BE784416
VERSION BE784416
KEYWORDS BE784416.1 GI:10205614
EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

1 (bases 1 to 853)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-rcmail.nih.gov

Tissue Procurement: DCM/DMP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNI at:

http://image.llnl.gov

Plate: L14M638 row: e column: 23

High quality sequence stop: 660.

Location/Qualifiers

1. 853

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3876862"

/issue_type="large cell carcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_68"

/note="Organ: lung; Vector: pCMV-SPORE; Site 1: NciI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 1.46e-46 Length: 853

ORIGIN

Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

Alignment Scores:

Pred. No.: 1.49e-46 Length: 870
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG740396 (1-870)

QY 1 MetGUAGAlaLeuAsnSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 71 ATGGAAAGGGCTGTGAACCTCACTCGAGCCCTCCGTGAGAGAGAGCCCTTGGAAACGC 130
QY 21 ATGProGUThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
DB 131 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACCACT 190
QY 41 AspSerThrThrSerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 191 GATTCCACCACTTCTTAATAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGAGCATG 250
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 251 TTCTCTCATTAACCTGGAATATGATGATTGATTAACAATCTGTCAAGAGGGCT 310
QY 81 ArgGlyValCysSerTyLeu 87
DB 311 CGAGGGGTGTGTTCTACTTA 331

RESULT 59

BU159911

LOCUS

DEFINITION AGENCOURT_7933863 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6144208

5', mRNA sequence.

ACCESSION BU159911 GI:22673821

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Homosapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homniidae; Homo.

1 (bases 1 to 870)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM13468 row: n column: 17

High quality sequence stop: 677.

Location/Qualifiers

1.870

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

ORIGIN

Average insert size 1.75 kb. Library constructed by Life Technologies."

Alignment Scores:

Pred. No.: 1.49e-46 Length: 870
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BU159911 (1-870)

QY 1 MetGUAGAlaLeuAsnSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 95 ATGGAAAGGGCTGTGAACCTCACTCGAGCCCTCCGTGAGAGAGAGCCCTTGGAAACGC 154
QY 21 ATGProGUThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
DB 155 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACCACT 214
QY 41 AspSerThrThrSerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 215 GATTCCACCACTTCTTAATAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGAGCATG 274
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 275 TTCTCTCATTAACCTGGAATATGATGATTGATTAACAATCTGTCAAGAGGGCT 334
QY 81 ArgGlyValCysSerTyLeu 87
DB 335 CGAGGGGTGTGTTCTACTTA 355

RESULT 60

BU169945

LOCUS

DEFINITION AGENCOURT_7913097 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6024760

5', mRNA sequence.

ACCESSION BU169945 GI:22683929

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Homosapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homniidae; Homo.

1 (bases 1 to 883)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: DCTD/DP/Gapzar

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM13235 row: m column: 17

High quality sequence stop: 413.

Location/Qualifiers

1.883

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

FEATURES

source

1.870

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6144208"

/tissue_type="retinoblastoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_67"

/note="Organ: eye; Vector: PCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.rst

Page 38

ORIGIN Average insert size 1.8 kb. Library constructed by Life Technologies. "

Alignment Scores:

Pred. No.: 1.52e-46 Length: 883
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BU169945 (1-883)

OY 1 MetGUArgAlaLeuAseSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 40 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCCTCGGGGAGGAGAGCGCTTGAGAACGC 99
OY 21 ArgProGluThrIleSerGluProIleThrTYrValAspLeuThrAsnGluGluThrThr 40
DB 100 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTCCTAACCAATGAGAAACAACCT 159
OY 41 AspSerThrIleSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 160 GATTCACCACTTCTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGCGAGCATG 219
OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 220 TTCTCTCATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTCAAGAGGGCT 279
OY 81 ArgGlyValCysSerTYrLeu 87
DB 280 CGAGGGGTGTGTTCTTACTTA 300

RESULT 61

BU179107 883 bp mRNA linear EST 04-SEP-2002
LOCUS BU179107
DEFINITION AGNCOURT 7984768 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6174958

5' mRNA sequence.

ACCESSION BU179107 GI:22693091

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 883)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LHAM13548 row: 0 column: 23
High quality sequence stop: 672.
Location/Qualifiers
1 883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="6174958"
/feature_type="cDNA_scaffold"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/notes="Organ: Uterus; Vector: pCMV-SPORT6; Site: 1: NCI,
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT."

ORIGIN Average insert size 2.1 kb. "

Alignment Scores:

Pred. No.: 1.52e-46 Length: 883
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BU179107 (1-883)

OY 1 MetGUArgAlaLeuAseSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 18 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCCTCGGGGAGGAGAGCGCTTGAGAACGC 77
OY 21 ArgProGluThrIleSerGluProIleThrTYrValAspLeuThrAsnGluGluThrThr 40
DB 78 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTCCTAACCAATGAGAAACAACCT 137
OY 41 AspSerThrIleSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 138 GATTCACCACTTCTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGCGAGCATG 197
OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 198 TTCTCTCATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTCAAGAGGGCT 257
OY 81 ArgGlyValCysSerTYrLeu 87
DB 258 CGAGGGGTGTGTTCTTACTTA 278

RESULT 62

CD251503 906 bp mRNA linear EST 22-MAY-2003
LOCUS CD251503
DEFINITION AGNCOURT 14212105 NIH_MGC_179 Homo sapiens cDNA clone

IMAGE:30385385 5' mRNA sequence.

ACCESSION CD251503 GI:31011969

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 906)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: NDMA452 row: 6 column: 18
High quality sequence stop: 588.
Location/Qualifiers
1 906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="30385385"
/feature_type="cDNA_scaffold"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/notes="TI and T5 phage resistances)"

/note="Organ: brain; Vector: PCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	1.58e-46	Length:	906
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CD251503 (1-906)

QY 1 MetGUAAGAlaLeuAnsSerTyRPhGluProProValGluGluSerAlaLeuGluArg 20
 DB 201 ATGAAAGGGCTCTGAACCTTCTGAGCTCCGGTGGAGAGAGGCCCTTGGAGAGCC 260
 QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThr 40
 DB 261 CGACCTGAACCATCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 320
 QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGlnAsnGlySerMet 60
 DB 321 GATTCACACACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGACG 380
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 381 TTCTCTCATTAACCTGGAATATTGATGATTAGTCTAAACAATCTGTCAAGAGGGCT 440
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 441 CGAGGGGTGTGTCTCTACTTA 461

RESULT 63

LOCUS

BG541819 937 bp mRNA linear EST 03-APR-2001
 BG541819 602569712F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694066 5',
 mRNA sequence.

ACCESSION

VERSION

BG541819.1 GI:13534052
 EST.

KEYWORDS

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLOUTCH Laboratories, Inc.
 cDNA Library Preparation: CLOUTCH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHCMS17 row: h column: 03
 High quality sequence scop: 714.
 Location/Qualifiers

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4694066"
 /lab_host="DH10B (TI phage-resistant)"

/clone.lib="NIH_MGC_77"
 /note="Organ: lung; Vector: pDNR-LTB (Clontech); Site 1:
 SfiI (ggcccctggcc); Site 2: SfiI (ggccattggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTAATGCG-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGGCGGCGCATGTG-dT (30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.65e-46	Length:	937
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BG541819 (1-937)

QY 1 MetGUAAGAlaLeuAnsSerTyRPhGluProProValGluGluSerAlaLeuGluArg 20
 DB 176 ATGAAAGGGCTCTGAACCTTCTGAGCTCCGGTGGAGAGAGGCCCTTGGAGAGCC 235
 QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThr 40
 DB 236 CGACCTGAACCATCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 295
 QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGlnAsnGlySerMet 60
 DB 296 GATTCACACACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGACG 355
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 356 TTCTCTCATTAACCTGGAATATTGATGATTAGTCTAAACAATCTGTCAAGAGGGCT 415
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 416 CGAGGGGTGTGTCTCTACTTA 436

RESULT 64

LOCUS

AL555333 948 bp mRNA linear EST 30-MAR-2004
 AL555333 AL555333 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DK007YK05 5-PRIME, mRNA sequence.

ACCESSION

VERSION

AL555333.3 GI:45860070
 EST.

KEYWORDS

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE

AUTHORS

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31277141.
 Contact: Genoscope

COMMENT

Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DK007AF03QPI&c=3474.r.

FEATURES
source
Location/Qualifiers
1. 948
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="CSDBK007YK05"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.67e-46 Length: 948
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x AL555333 (1-948)

QY 1 MetGluArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 179 ATGGAAAGGCGCTGAACTCTGAACTTCGAGCGCTCGGAGGAGAGAGCGCTTGAGACGC 238

QY 21 ArgProGluThrIleSerGluProValAspLeuThrAsnGluGluThr 40
Db 239 CGACCTGAACCATCTCTGAGCCCAAGACCATGTGACCTAAACCATGAGAAACAACACT 298

QY 41 AsperThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 239 GATTCACCACTTCTAAATCAAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATG 358

QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 359 TTCCTCTCATTAACCTGGAATATTGATGATTGATCTAAACAATCTGTCAAGAGGCT 418

QY 81 ArgGlyValCysSerTyLeu 87
Db 419 CGAGGGGTGTCTCTACTTA 439

RESULT 65
B1161201 959 bp mRNA linear EST 05-JUL-2001
LOCUS 60286565921 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019639 5',
DEFINITION mRNA sequence.
ACCESSION B1161201
VERSION B1161201.1 GI:14621202
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 959)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1835 row: e column: 16
High quality sequence stop: 551.

FEATURES
source
Location/Qualifiers
1. 959
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5019639"
/issue="IMAGE:5019639"
/issue_type="epithelioid carcinoma cell line"
/lab_host="VH10B (phage-resistant)"
/clone_lib="NIH-MGC_42"
/note="Organ: pancreas; vector: pORF7; site_1: XhoI;
site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald W. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library."

ORIGIN
Alignment Scores:
Pred. No.: 1.7e-46 Length: 959
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x B1161201 (1-959)

QY 1 MetGluArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 178 ATGGAAAGGCGCTGAACTCTGAACTTCGAGCGCTCGGAGGAGAGAGCGCTTGAGACGC 237

QY 21 ArgProGluThrIleSerGluProValAspLeuThrAsnGluGluThr 40
Db 238 CGACCTGAACCATCTCTGAGCCCAAGACCATGTGACCTAAACCATGAGAAACAACACT 297

QY 41 AsperThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 298 GATTCACCACTTCTAAATCAAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATG 357

QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 358 TTCCTCTCATTAACCTGGAATATTGATGATTGATCTAAACAATCTGTCAAGAGGCT 417

QY 81 ArgGlyValCysSerTyLeu 87
Db 418 CGAGGGGTGTCTCTACTTA 438

RESULT 66
B1161201 972 bp mRNA linear EST 05-FEB-2002
LOCUS 6445782 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587154
DEFINITION 5', mRNA sequence.
ACCESSION B1161201
VERSION B1161201.1 GI:18517868
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 972)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLM12356 row: d column: 03
 High quality sequence stop: 707.
 Location/Qualifiers

FEATURES

1..972
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5587154"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (Phage-resistant)"
 /clone_1ib="NIH_MGC_92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1.73e-46 Length: 972
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BM468826 (1-972)

QY 1 MetGUAAGAlaLeuAnsSerTYrPhgIuPProProValGluGluSerAlaLeuGluAarg 20
 DB 55 ATGGAAGAGGGCTCTGAACCTCTTCACTCGAGCCTCCGGTGAAGAGAGCCCTTGGAACGC 114
 QY 21 ATGProGluThrIleSerGluProlySerThyValAspLeuThraAsnGluGluThrThr 40
 DB 115 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 174
 QY 41 AApSerThrThrSerIleIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 175 GATTCACCACTCTTAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGCGACATG 234
 QY 61 PheSerLeuIleThrThraAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluAargAla 80
 DB 235 TTCTCTCATTAACCTGAATATGATGATTAAGATCAACATCTGTGAGAGAGGGCT 294
 QY 81 ATGGLyValCyseSerTyLeu 87
 DB 295 CGAGGGGTGTCTTCTACTTA 315

RESULT 67
 BX338160 981 bp mRNA linear EST 08-APR-2004
 LOCUS BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1056YC23.5-PRIME, mRNA sequence.
 ACCESSION BX338160
 VERSION BX338160.2 GI:46283046
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 981)
 REFERENCE
 AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 2, 2003 this sequence version replaced gi:30345671.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna78=CS0D1056AB12QPI&c=3474.r>.

FEATURES

1..981
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1056YC23"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 1.75e-46 Length: 981
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BX338160 (1-981)

QY 1 MetGUAAGAlaLeuAnsSerTYrPhgIuPProProValGluGluSerAlaLeuGluAarg 20
 DB 173 ATGGAAGAGGGCTCTGAACCTCTTCACTCGAGCCTCCGGTGAAGAGAGCCCTTGGAACGC 232
 QY 21 ATGProGluThrIleSerGluProlySerThyValAspLeuThraAsnGluGluThrThr 40
 DB 233 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 292
 QY 41 AApSerThrThrSerIleIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 293 GATTCACCACTCTTAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGCGACATG 352
 QY 61 PheSerLeuIleThrThraAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluAargAla 80
 DB 353 TTCTCTCATTAACCTGAATATGATGATTAAGATCAACATCTGTGAGAGAGGGCT 412
 QY 81 ATGGLyValCyseSerTyLeu 87
 DB 413 CGAGGGGTGTCTTCTACTTA 433

RESULT 68
 BE892886 995 bp mRNA linear EST 20-OCT-2000
 LOCUS BE892886
 DEFINITION 601435730F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920790 5', mRNA sequence.
 ACCESSION BE892886
 VERSION BE892886.1 GI:10353510
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 995)
 REFERENCE
 AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1998)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Jocyte Genotyping, Inc.
Cloned through the I.M.A.G.E. Consortium (LNL) at:
<http://image.lnl.gov>
Plate: L1M9752 row: 1 column: 07
High quality sequence stop: 573.

FEATURES
source

1. 995
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3920790"
/issue_type="neurotic melanoma"
/lab_host="MDH08 (MDH08 drug-resistant)"
/clone_1ib="NIH-MGC_12"
/note="Organ: Skin; Vector: pCMV-SPORT6; Site: 1: NotI,
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 1.78e-46 Length: 995
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BB892886 (1-995)

QY 1 MetGUAAGAlaLeuAaSerTYrPheGluProProValAGluGuaAlaLeuGuaG 20
Db 189 ATGGAAAGGGCTCTGAACCTCTCTGAGACCTCGGAGGAGAGAGAGAGAGAGAG 248
QY 21 ArgProGluThrIleSerGluProLyThrTYrValAAspLeuThrAaGluGluThr 40
Db 249 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAACAACT 308
QY 41 AspSerThrSerTYrIleSerProSerGluAAspThrGluGluGluAaGlySerMet 60
Db 309 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 368
QY 61 PheSerLeuIleThrTYrAaAaAAspGlyLeuAAspLeuAaAaAaAaAaAaAaAa 80
Db 369 TTCTCTCATTAATCTGAAATATGATGATTGATTAATTAACATCTGTCAAGAGGCT 428
QY 81 ArgGlyValCysSerTYrLeu 87
Db 429 CGAGGGGTGTGTTCTTACTTA 449

RESULT 69

EX337141

LOCUS

EX337141

DEFINITION

EX337141

ACCESSION

EX337141

VERSION

EX337141.2

KEYWORDS

EST

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 1018)

Full-length cDNA libraries and normalization

On May 2, 2003 this sequence version replaced gi:30337585.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdnats=OSODI036DE01QPlc=3474.r>.

FEATURES
source

1. 1018
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OSODI036YU02"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1.84e-46 Length: 1018
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BX337141 (1-1018)

QY 1 MetGUAAGAlaLeuAaSerTYrPheGluProProValAGluGuaAlaLeuGuaG 20
Db 150 ATGGAAAGGGCTCTGAACCTCTCTGAGACCTCGGAGGAGAGAGAGAGAGAGAG 209
QY 21 ArgProGluThrIleSerGluProLyThrTYrValAAspLeuThrAaGluGluThr 40
Db 210 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAACAACT 259
QY 41 AspSerThrSerTYrIleSerProSerGluAAspThrGluGluGluAaGlySerMet 60
Db 270 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 329
QY 61 PheSerLeuIleThrTYrAaAaAAspGlyLeuAAspLeuAaAaAaAaAaAaAaAa 80
Db 330 TTCTCTCATTAATCTGAAATATGATGATTGATTAATTAACATCTGTCAAGAGGCT 389
QY 81 ArgGlyValCysSerTYrLeu 87
Db 390 CGAGGGGTGTGTTCTTACTTA 410

RESULT 70

BM554324

LOCUS

BM554324

DEFINITION

BM554324

ACCESSION

BM554324

VERSION

BM554324.1

KEYWORDS

EST

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 1035)

Full-length cDNA libraries and normalization

On May 2, 2003 this sequence version replaced gi:30337585.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE

CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.jnl.gov>
 Plate: LLM12760 row: k column: 11
 High quality sequence stop: 738.

FEATURES

source

1..1035

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5742466"

/tissue_type="medulla"

/lab_host="DH10B"

/clone_1ib="NIH_MGC_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 1,88e-46 Length: 1035
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BMS54324 (1-1035)

QY 1 MetGUAAGAlaLeuAnsSerTyrrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 332 ATGGAAGGGCTCTGAACCTCTTCCGAGCTCCGGTGAGAGAGCCCTTGGAACCC 391
 QY 21 ATGPGGluThrIleSerGluProLyThrTyrrValAspLeuThrAsnGluGluThrThr 40
 DB 392 CCACTGAAACCATCTCTAGCCCAAGACCTTATGTTGACCTTAACATAGAAACAACACT 451
 QY 41 AspSerThrThrSerLySileSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 452 GATTCACACCTTTTAAATCAGCCCATCTGAAGAACTCAGCAAGAAATGGCAGCATG 511
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 512 TTCTCTCATTAACCTGAAATATGATGATTAGATTAAACAATCTGTCAAGAGGGCT 571
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 572 CGAGGGGTGTCTCTACTTA 592

RESULT 71

LOCUS BX337905 1067 bp mRNA linear EST 07-APR-2004
 DEFINITION BX337905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CSOD1052YNI3 5-PRIME, mRNA sequence.

ACCESSION

BX337905 GI:46273926

VERSION

BX337905.2 GI:46273926

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 1067)
 L.I.W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 2, 2003 this sequence version replaced gi:30339657.

CONTACT

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CSOD1052CG070P1&c=3474.r>.

FEATURES

source

1..1067

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOD1052YNI3"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1,95e-46 Length: 1067
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BX337905 (1-1067)

QY 1 MetGUAAGAlaLeuAnsSerTyrrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 184 ATGGAAGGGCTCTGAACCTCTTCCGAGCTCCGGTGAGAGAGCCCTTGGAACCC 243
 QY 21 ATGPGGluThrIleSerGluProLyThrTyrrValAspLeuThrAsnGluGluThrThr 40
 DB 244 CCACTGAAACCATCTCTAGCCCAAGACCTTATGTTGACCTTAACATAGAAACAACACT 303
 QY 41 AspSerThrThrSerLySileSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 304 GATTCACACCTTTTAAATCAGCCCATCTGAAGAACTCAGCAAGAAATGGCAGCATG 363
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 364 TTCTCTCATTAACCTGAAATATGATGATTAGATTAAACAATCTGTCAAGAGGGCT 423
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 424 CGAGGGGTGTCTCTACTTA 444

RESULT 72

LOCUS BX444691 1081 bp mRNA linear EST 04-MAY-2004
 DEFINITION BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 CSODN005YNI02 5-PRIME, mRNA sequence.

ACCESSION

BX444691 GI:47009162

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 1081)

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.rst

Page 44

AUTHORS
TITLE
JOURNAL
COMMENT

L.I.W.B., Gruber, C., Jesssee, J., and Polayes, D.
Full-length cDNA libraries and normalization
On May 15, 2003 this sequence version replaced g1.30780264.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CSODN005D01Q1P1&c=3474.r.
Location/Qualifiers
1..1081
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN005YNO2"
/issue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_1ib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 1.99e-46 Length: 1081
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BX444691 (1-1081)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 186 ATGAAAGGGCTCTGAATCTTCACTTCAGAGCTCCGGTGAAGAGAGAGCCCTTGGAACGC 245
QY 21 ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThr 40
DB 246 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAACACT 305
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 306 GATTCACACCACTCTAAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGGCAGCATG 365
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnIleuSerGluArgAla 80
DB 366 TTCTCTCATTAACCTGGAATATGATGATTGAATCAAAACAATCTGTCAGAGAGGCT 425
QY 81 ArgGlyValCysSerTyrLeu 87
DB 426 CGAGGGGTGTGTTCTTACTTA 446

RESULT 73
LOCUS DQ049205 1089 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens TTRAP gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ049205
VERSION DQ049205.1 GI:66902404
KEYWORDS GSS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
COMMENT
JOURNAL
COMMENT

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 1089)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(ex) PLoS Biol. 3 (6), E170 (2005)
2 (bases 1 to 1089)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-May-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
Location/Qualifiers
1..1089
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
1..>1089
/gene="TTRAP"
/locus_tag="HC17203"

FEATURES

source

ORIGIN

gene

Alignment Scores:

Pred. No.: 2.01e-46 Length: 1089
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x DQ049205 (1-1089)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 160 ATGAAAGGGCTCTGAATCTTCACTTCAGAGCTCCGGTGAAGAGAGAGCCCTTGGAACGC 219
QY 21 ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThr 40
DB 220 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAACACT 279
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 280 GATTCACACCACTCTAAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGGCAGCATG 339
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnIleuSerGluArgAla 80
DB 340 TTCTCTCATTAACCTGGAATATGATGATTGAATCAAAACAATCTGTCAGAGAGGCT 399
QY 81 ArgGlyValCysSerTyrLeu 87
DB 400 CGAGGGGTGTGTTCTTACTTA 420

RESULT 74
LOCUS BM555041 1103 bp mRNA linear EST 20-FEB-2002
DEFINITION AGNCCOURT_6545705 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737150
5', mRNA sequence.
ACCESSION BM555041
VERSION BM555041.1 GI:18795166
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 1103)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strusberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
Place: LLM12746 row: m column: 23
High quality sequence stop: 678.
Location/Qualifiers
1..1103

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5737150"
/tissue="quodanal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 2,046-46 Length: 1103
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BM555041 (1-1103)

OY 1 MetGUAAGAlaLeuAenSerTyRheGluProProValAGluGluSerAlaLeuGluArg 20
DB 189 ATGAAAGGGCTCTGAACCTCTACTTCAGGCTCCGGTGAAGAGAGCGCTTGAAAGCC 248
OY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
DB 249 CGACCTGAACCACTCTGAGCCCAAGACCTATGTGACTTAACCAATGAAGAAACAAC 308
OY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 309 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 368
OY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 369 TTCTCTCATTAACCTGGAATATGATGATTAATCAATCAATCTGTCAAGAGGGCT 428
OY 81 ArgGlyValCysSerTyLeu 87
DB 429 CGAGGGGTGTGTCTCTACTTA 449

RESULT 75
LOCUS CR601303 1168 bp mRNA linear HTC 21-JUL-2004
DEFINITION Full-length cDNA clone CS0DN005YN02 of Adult brain of Homo sapiens (human).
ACCESSION CR601303
VERSION CR601303.1 GI:50482110
KEYWORDS HTC; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1168)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Feng Liang Email: fliang@lifestech.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Paraday Avenue
2 (bases 1 to 1168)
Genoscope.
Direct Submission

REFERENCE 2 (bases 1 to 1168)
AUTHORS Genoscope.
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : segret@genoscope.cns.fr)
JOURNAL - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

COMMENT

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN005YN02"
/tissue_type="Adult brain"
/plasmid="pCMVSPORT_6"
Location/Qualifiers
1..1168

ORIGIN

Alignment Scores:
Pred. No.: 2,26-46 Length: 1168
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR601303 (1-1168)

OY 1 MetGUAAGAlaLeuAenSerTyRheGluProProValAGluGluSerAlaLeuGluArg 20
DB 185 ATGAAAGGGCTCTGAACCTCTACTTCAGGCTCCGGTGAAGAGAGCGCTTGAAAGCC 244
OY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
DB 245 CGACCTGAACCACTCTGAGCCCAAGACCTATGTGACTTAACCAATGAAGAAACAAC 304
OY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 305 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 364
OY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 365 TTCTCTCATTAACCTGGAATATGATGATTAATCAATCAATCTGTCAAGAGGGCT 424
OY 81 ArgGlyValCysSerTyLeu 87
DB 425 CGAGGGGTGTGTCTCTACTTA 445

RESULT 76
LOCUS BM553049 1192 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6542413 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742798 5', mRNA sequence.
ACCESSION BM553049
VERSION BM553049.1 GI:18791437
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

Thu Mar 16 10:39:27 2006

US-10-757-745-2_copy_34_140.txt

Page 46

REFERENCE 1 (bases 1 to 1192)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM12761 row: 1 column: 07
High quality sequence stop: 747.

FEATURES

source

1..1192
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742798"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_11b="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 2,266-46 Length: 1192
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BM53049 (1-1192)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 217 ATGAAAGGGCTCTGAACCTTACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAAAGC 276
QY 21 ArgProGluThrIleSerGluProValThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 277 CGACCTGAAACCATCTCTGAGCCCAAGACCTTGTGTACCAACCAATGAGAAACAAC 336
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGlnGln 60
DB 337 GATTCACACACTTCTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGCGACGATG 396
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 397 TTCTCTCATTAACCTGGAATTAATGATTAAGTCTAAACAATCTGTCAAGAGGGCT 456
QY 81 ArgGlyValCysSerTyrLeu 87
DB 457 CAGAGGGGTGTCTTCTACTTA 477

RESULT 77
LOCUS CR592636 1620 bp mRNA linear HTC 21-JUL-2004
DEFINITION Full-length cDNA clone CS0DM007YB11 of Petal liver of Homo sapiens
ACCESSION CR592636
VERSION CR592636.1 GI:50473443
KEYWORDS HTC; CNSLT_CDNA.

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 1620)
AUTHORS Li, W.B., Gruber, C., Jeesee, J. and Polyses, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@life.uci.edu
<http://fulllength.invitrogen.com/> invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1620)

REFERENCE 2 (bases 1 to 1620)
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of invitrogen.

FEATURES

source

1..1620
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YB11"
/tissue_type="fetal liver"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 3,386-46 Length: 1620
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR592636 (1-1620)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 103 ATGAAAGGGCTCTGAACCTTACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAAAGC 162
QY 21 ArgProGluThrIleSerGluProValThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 163 CGACCTGAAACCATCTCTGAGCCCAAGACCTTGTGTACCAACCAATGAGAAACAAC 222
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGlnGln 60
DB 223 GATTCACACACTTCTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGCGACGATG 282
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 283 TTCTCTCATTAACCTGGAATTAATGATTAAGTCTAAACAATCTGTCAAGAGGGCT 342
QY 81 ArgGlyValCysSerTyrLeu 87
DB 343 CAGAGGGGTGTCTTCTACTTA 363

RESULT 78
LOCUS CR597293 1894 bp mRNA linear HTC 21-JUL-2004
DEFINITION Full-length cDNA clone CS0DK007YK05 of HeLa cells Cot 25-normalized
ACCESSION CR597293
VERSION CR597293.1 GI:50478100
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1894)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1894)
REFERENCE 2 (bases 1 to 1894)
AUTHORS Direct Submission
TITLE Genoscope.
JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK007YK05"
/tissue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 4,14e-46 Length: 1894
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x CR597293 (1-1894)
QY 1 MetGUATGAlaLeuanserTyrPheGluProProValIGluGluSerAlaLeuGluArg 20
DB 178 ATGGAAGGGCTCTGAACCTCTTCACTCCGCTCGAGAGAGAGCCCTTGAAGCC 237
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 238 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 297
QY 41 AspSerThrThrSerIleValIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 238 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATTAACACAGAAATGCGCAGCAG 357
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 358 TTCTCTCATTAACCTGGAATATTGATGATTAAGATTAACAATCTGTCAAGAGAGGCT 417
QY 81 ArgGlyValCysSerTyrLeu 87
DB 418 CGAGGGGTGTCTTCTACTTA 438
RESULT 79
LOCUS CR595644 1909 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSOD1052YN13 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR595644
VERSION CR595644.1 GI:50476451
KEYWORDS HTC, CNSUT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 1909)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1909)
REFERENCE 2 (bases 1 to 1909)
AUTHORS Direct Submission
TITLE Genoscope.
JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1909
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1052YN13"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 4,19e-46 Length: 1909
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x CR595644 (1-1909)
QY 1 MetGUATGAlaLeuanserTyrPheGluProProValIGluGluSerAlaLeuGluArg 20
DB 184 ATGGAAGGGCTCTGAACCTCTTCACTCCGCTCGAGAGAGAGCCCTTGAAGCC 243
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 244 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 303
QY 41 AspSerThrThrSerIleValIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 304 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATTAACACAGAAATGCGCAGCAG 363
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 364 TTCTCTCATTAACCTGGAATATTGATGATTAAGATTAACAATCTGTCAAGAGAGGCT 423
QY 81 ArgGlyValCysSerTyrLeu 87
DB 424 CGAGGGGTGTCTTCTACTTA 444
RESULT 80
LOCUS AV717253 581 bp mRNA linear EST 16-OCT-2000
DEFINITION AV717253 DCB Homo sapiens cDNA clone DCBMA04 5', mRNA sequence.
ACCESSION AV717253
VERSION AV717253.1 GI:10814405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,

Sen, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,
Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Cheng, Z., and Han, Z.
Homo sapiens cDNA DB clones
Unpublished (2000)
Contact: Zengqiang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBMA04"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
/clone_id="DCB"
/note="Vector: pTRIPlex2; Site_1: sf1A; Site_2: sf1B"

ORIGIN

Alignment Scores:
Pred. No.: 2.13e-46 Length: 581
Score: 445.00 Matches: 86
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 98.9% Mismatches: 0
Query Match: 99.3% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AV1717253 (1-581)

QY 1 MetGUAAGAlaleuAenSerTYrPheGluProProValAGluGluSerAlaleuGluArg 20
DB 3 ATGGAAGGCTCTCGAAGCTCTACTTCGAGCTCCGGTGGAGGAGACCGCTTGGAAGCG 62
QY 21 ArgProGluThrIleSerGluProLysThrTYrValAepLeuThrAngGluGluThrThr 40
DB 63 CGACCTGAAACCATCTCTGAGCCCAAGCCTATGTTGACCTPAACCAATGAAAGAACT 122
QY 41 AepSerThrThrSerLysIleSerProSerGluAepThrGluGluGluAngLysSerMet 60
DB 123 GATCCACCACTCTTAATAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGCGACGATG 182
QY 61 PheSerLeuIleThrTPAenIleAepGlyLeuAepLeuAenAenLeuSerGluArgAla 80
DB 183 TTCTCTCATTTACTCGAATATTGATGATTAAGTCTTAACCAATCTGTCAAGAGGGCT 242
QY 81 ArgGlyValCysSerTYrLeu 87
DB 243 CGAGGGGTGTCTTCTTCTTA 263

RESULT 81

BP234218 582 bp mRNA linear EST 15-SEP-2004
LOCUS BP234218 Sugano cDNA library, coronary artery endothelial cell Homo
DEFINITION sapiens cDNA clone HCR02378, mRNA sequence.
ACCESSION BP234218
VERSION BP234218.1 GI:52107128
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous

JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
COMMENT 15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ime.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES

Source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR02378"
/issue_type="coronary artery"
/cell_type="endothelial cell"
/clone_id="Sugano cDNA library, coronary artery
endothelial cell"

ORIGIN

Alignment Scores:
Pred. No.: 2.87e-46 Length: 582
Score: 444.00 Matches: 86
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 98.9% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP234218 (1-582)

QY 1 MetGUAAGAlaleuAenSerTYrPheGluProProValAGluGluSerAlaleuGluArg 20
DB 187 ATGGAAGGCTCTCGAAGCTCTACTTCGAGCTCCGGTGGAGGAGACCGCTTGGAAGCG 246
QY 21 ArgProGluThrIleSerGluProLysThrTYrValAepLeuThrAngGluGluThrThr 40
DB 247 CGACCTGAAACCATCTCTGAGCCCAAGCCTATGTTGACCTPAACCAATGAAAGAACT 306
QY 41 AepSerThrThrSerLysIleSerProSerGluAepThrGluGluGluAngLysSerMet 60
DB 307 GATTCACCACTCTTAATAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGCGACGATG 366
QY 61 PheSerLeuIleThrTPAenIleAepGlyLeuAepLeuAenAenLeuSerGluArgAla 80
DB 367 TTCTCTCATTTACTCGAATATTGATGATTAAGTCTTAACCAATCTGTCAAGAGGGCT 426
QY 81 ArgGlyValCysSerTYrLeu 87
DB 427 CGAGGGGTGTCTTCTTCTTA 447

RESULT 82

BP233592 582 bp mRNA linear EST 15-SEP-2004
LOCUS BP233592 Sugano cDNA library, coronary artery endothelial cell Homo
DEFINITION sapiens cDNA clone HCR00774, mRNA sequence.
ACCESSION BP233592
VERSION BP233592.1 GI:52106502
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysnuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR00774"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_lib="Sugano cDNA library, coronary artery
endothelial cell"

ORIGIN

Alignment Scores:

Pred. No.:	3,85e-46	Length:	582
Score:	443.00	Matches:	86
Percent Similarity:	98.9%	Conservative:	0
Best Local Similarity:	98.9%	Mismatches:	1
Query Match:	98.9%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BP233592 (1-582)

QY 1 MetGUAAGAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 175 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGAAGAGAGCCCTTGAAACGC 234
QY 21 ATGPGGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 235 CGACCTGAACACATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAT 294
QY 41 AAPPserThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 295 GATTCACACACTCTCAAAATCAGCCCATCTGAAGATCTCAGCAAGAAACGACGACATG 354
QY 61 PheSerIleuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 355 TTCTCTCATTAACCTGGAATATGATGATTGATTAACAATCTGTCAAGAGAGGCT 414
QY 81 ATGGLYValCySeSerTyrLeu 87
DB 415 CGAGGGGTGTCTTCTACTTA 435

RESULT 83

BP262485

LOCUS BP262485 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION clone HS107111, mRNA sequence.

ACCESSION BP262485.1 GI:52177716

VERSION BP262485.1 GI:52177716

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 572)

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki

Department of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysnuzuki@ims.u-tokyo.ac.jp.

FEATURES

source
1..572
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="HS107111"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:	9.11e-46	Length:	572
Pred. No.: <td>440.00<td>Matches:<td>85</td></td></td>	440.00 <td>Matches:<td>85</td></td>	Matches: <td>85</td>	85
Score: <td>440.00<td>Conservative:<td>1</td></td></td>	440.00 <td>Conservative:<td>1</td></td>	Conservative: <td>1</td>	1
Percent Similarity: <td>100.0%</td> <td>Mismatches:<td>0</td></td>	100.0%	Mismatches: <td>0</td>	0
Best Local Similarity: <td>98.8%</td> <td>Indels:<td>0</td></td>	98.8%	Indels: <td>0</td>	0
Query Match: <td>98.2%</td> <td>Gaps:<td>0</td></td>	98.2%	Gaps: <td>0</td>	0
DB: <td>3</td> <td></td> <td></td>	3		

US-10-757-745-2_COPY_54_140 (1-87) x BP262485 (1-572)

QY 2 GUATGAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 21
DB 119 CAGAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGAAGAGAGCCCTTGAAACGCCA 178
QY 22 ProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThrThr 41
DB 179 CCTGAACACATCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAATGAT 238
QY 42 SerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
DB 239 TCTCATTAACCTGGAATATGATGATTGATTAACAATCTGTCAAGAGAGGCTCGA 298
QY 62 SerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 81
DB 299 TTCTCATTAACCTGGAATATGATGATTGATTAACAATCTGTCAAGAGAGGCTCGA 358
QY 82 GLYValCySeSerTyrLeu 87
DB 359 GGGGTGTGTCTTCTACTTA 376

RESULT 84

BP263516

LOCUS BP263516 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION clone HS11929, mRNA sequence.

ACCESSION BP263516.1 GI:52178747

VERSION BP263516.1 GI:52178747

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 582)

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki

Department of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysnuzuki@ims.u-tokyo.ac.jp.

FEATURES

source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS11929"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 9.32e-46 Length: 582

Score: 440.00 Matches: 85
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 98.8% Mismatches: 0
Query Match: 98.2% Indels: 0
Gaps: 0
DB: 3

US-10-757-745-2_COPY_54_140 (1-87) x BP263516 (1-582)

QY 2 GluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGuaArg 21
DB 129 CAGAGGCTCTGAAGCTCTGAGCCCTCCGGTGGAGAGAGCGCTTGGAACCCCGA 188
QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAsp 41
DB 189 CCGAAGACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACTGAT 248
QY 42 SerThrThrSerTyrIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
DB 249 TCCACACACTCTAAATCAAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTTCC 308
QY 62 SerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
DB 309 TCTCTCATTTACCTGAAATATTGATGATTAGATCTTAAACAATCTGTGAGAGAGGCTCGA 368
QY 82 GlyValCysSerTyrLeu 87
DB 369 GGGGTGTGTCTCTACTTA 386

RESULT 85
BF977971 626 bp mRNA linear EST 22-JAN-2001
LOCUS 602148451P1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4307317 5',
DEFINITION mRNA sequence.
ACCESSION BF977971
VERSION BF977971.1 GI:12345186
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 626)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Clontech Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: ILCM1177 row: e column: 14
High quality sequence stop: 614.
Location/Qualifiers

FEATURES

source
1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4307317"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH MGC 62"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (ggcgccctggcc); Site 2: SfiI (ggccatcaggcc)
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCAGAGCCAGCGCCACACATG-dT(30)BN-3
sequence: 5'-ATTCAGAGCCAGCGCCACACATG-dT(30)BN-3
(where B = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies

ORIGIN

Alignment Scores:

Pred. No.: 1,02e-45
Score: 440.00
Percent Similarity: 100.0%
Best Local Similarity: 97.7%
Query Match: 96.2%
DB: 2

US-10-757-745-2_COPY_54_140 (1-87) x BF977971 (1-626)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGuaArg 20
DB 174 ATGGAAGGCTCTGAAGCTCTGAGCCCTCCGGTGGAGAGAGCGCTTGGAACCCCGA 223
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAsp 40
DB 234 CAGCTGAAGACCATCTGAGCCCAAGACCTATGTTGACCTTACCAATGAAGAAACAACT 293
QY 41 AspSerThrThrSerTyrIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 294 GATTCACACACTCTAAATCAAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTTCC 353
QY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 354 TCTCTCATTTACCTGAAATATTGATGATTAGATCTTAAACAATCTGTGAGAGGCTCGA 413
QY 81 ArgGlyValCysSerTyrLeu 87
DB 414 CAGAGGTGTGTCTCTACTTA 434

RESULT 86
BX358707 942 bp mRNA linear EST 08-APR-2004
LOCUS BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1042YL19 5-PRIME, mRNA sequence.
ACCESSION BX358707
VERSION BX358707.2 GI:46306560
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 942)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30378261.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-ClonDI (dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0D1042CP10P1ac=3474.r.
Location/Qualifiers

FEATURES

source
1..942
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1042YL19"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"

contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	1,75e-45	Length:	942
Score:	440.00	Matches:	85
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	98.8%	Mismatches:	0
Query Match:	98.2%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BM358707 (1-942)

QY 2 GUAAGALALEUANSerTYrPheGluProProValGluGluSerAlaLeuGluArg 21
 DB 32 CAGAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGAAGAGCGCCTTGAGAGCCGA 91
 QY 22 ProGluThrIleSerGluProIleThrTYrValaPleuThrAsnGluGluThrAsp 41
 DB 92 CCGAAGACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAATGAT 151
 QY 42 SerThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
 DB 152 TCACACCATCTTAAATACGCCCATCTGAAGATCTCAGCAGAAAGAAATGCGACATGTT 211
 QY 62 SerIleuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 81
 DB 212 TCTCATTAACCTGGAATATGATGATTAATCTTAACAATCTGTCAAGAGGGCTGCA 271
 QY 82 GYValCYseSerTYrLeu 87
 DB 272 GGGGTGTCTCTACTTA 289

RESULT 87

BM926092 1046 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT_6649780 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5764440
 DEFINITION 5', mRNA sequence.

ACCESSION BM926092
 VERSION BM926092.1 GI:19376471
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1046)
 NIH-MGC <http://mgs.nci.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-rmail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing By: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM12817 row: 0 column: 01
 High quality sequence start: 4
 High quality sequence stop: 632.
 Location/Qualifiers

FEATURES

source

1. 1046
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5764440"
 /lab_host="DH10B"
 /clone_11b="NIH_MGC_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2.01e-45	Length:	1046
Score:	440.00	Matches:	85
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	98.8%	Mismatches:	0
Query Match:	98.2%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BM926092 (1-1046)

QY 2 GUAAGALALEUANSerTYrPheGluProProValGluGluSerAlaLeuGluArg 21
 DB 36 CAGAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGAAGAGCGCCTTGAGAGCCGA 95
 QY 22 ProGluThrIleSerGluProIleThrTYrValaPleuThrAsnGluGluThrAsp 41
 DB 96 CCGAAGACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAATGAT 155
 QY 42 SerThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
 DB 156 TCACACCATCTTAAATACGCCCATCTGAAGATCTCAGCAGAAAGAAATGCGACATGTT 215
 QY 62 SerIleuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 81
 DB 216 TCTCATTAACCTGGAATATGATGATTAATCTTAACAATCTGTCAAGAGGGCTGCA 275
 QY 82 GYValCYseSerTYrLeu 87
 DB 276 GGGGTGTCTCTACTTA 293

RESULT 88

CR602029 1743 bp mRNA linear HTC 21-JUL-2004
 LOCUS CR602029 Full-length cDNA clone CSDDI042Y119 of Placenta Cot 25-normalized
 DEFINITION of Homo sapiens (human).

ACCESSION CR602029
 VERSION CR602029.1 GI:50482836
 KEYWORDS HTC; CNSLT_cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1743)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 Unpublished
 CONTACT: Feng Liang Email: fliang@lifestech.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1743)
 Genoscope.
 Direct Submission
 Submitted (20-JUL-2004) Genoscope (E-mail: segregenoscope.cns.fr
 BP 191 91006 Evry cedex - FRANCE)
 Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 Location/Qualifiers

REFERENCE

AUTHORS
 TITLE
 JOURNAL

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 Location/Qualifiers

SOURCE

1..1743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001047113"
/issue_type="placenta"
/plasmid="PCMVSPORT_5"

ORIGIN

Alignment Scores:
Pred. No.: 3,926-45 Length: 1743
Score: 440.00 Matches: 85
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 98.8% Mismatches: 0
Query Match: 98.2% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CRE02029 (1-1743)

QY 2 GUARGALAEUAASERTYYPHEGLUPROPROVALGUGLUSERALAEUGLUAARG 21
::: 32 CAGAGGGCTCTGAACCTCTACCTCGAGCTCCGGTGAAGAGAGCGCTTGAAACCGCA 91
QY 22 Progluthrilesergluprolyserthryvalaspueuthraenglugluthrthrap 41
DB 92 CCGAACAACATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAAGAACATGAT 151
QY 42 Serthrhserlyleaserprosergluasprthrglnglnglnglnglnglnglysermetphe 61
DB 153 TCCACACCTCTTAAATCAAGCCCATCTGAAGATCTCAGCAAGAAATGCGACAGCATGTTG 211
QY 62 Serleuilethrtipaanileapglyleuaapleuaenleuasergluargalaarg 81
DB 212 TCTCTCATTTACCTGGAAATATGATGATTAATGATCTTAAACATCTGTCAAGAGGGCTCGA 271
QY 82 GLYVALCYSESTYRLEU 87
DB 272 GGGGTGTGCTCTACTTA 289

RESULT 89
AUI39147 752 bp mRNA linear EST 02-AUG-2002
LOCUS AUI39147 PLACE1 Homo sapiens cDNA clone PLACE1010031 5', mRNA
DEFINITION AUI39147
ACCESSION AUI39147
VERSION AUI39147
KEYWORDS AUI39147.1 GI:11000668
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 752)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isegai,T.

REFERENCE

TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isegai
Genomics Laboratory
Helix Research Institute
153-3 Yana, Kizarezu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'- and one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

1..752
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="PLACE1010031"
/issue_type="placenta"
/clone_type="PLACE1"
/note="vector: pM18SPJ3"

ORIGIN

Alignment Scores:
Pred. No.: 1,756-45 Length: 752
Score: 439.00 Matches: 86
Percent Similarity: 98.9% Conservative: 0
Best Local Similarity: 98.9% Mismatches: 1
Query Match: 98.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AUI39147 (1-752)

QY 1 Metgluargalaeuaasertyyphegluproprovalgugluseralaeugluarg 20
DB 160 ATGAAAGGCTCTGAACCTCTACCTCGAGCTCCGATGAGAGAGCGCTTGAAACGC 219
QY 21 Argprogluthrilesergluprolyserthryvalaspueuthraenglugluthrthrap 40
DB 220 CGACCTGAACAACATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAAGAACACT 279
QY 41 Aspserthrhserlyleaserprosergluasprthrglnglnglnglnglnglnglysermetphe 60
DB 280 GATTCACACCTCTTAAATCAAGCCCATCTGAAGATCTCAGCAAGAAATGCGACAGCATG 339
QY 61 Pheaserleuilethrtipaanileapglyleuaapleuaenleuasergluargalaarg 80
DB 340 TTTCTCTCATTTACCTGGAAATATGATGATTAATGATCTTAAACATCTGTCAAGAGGGCT 399
QY 81 ARGGLYVALCYSESTYRLEU 87
DB 400 CGAGGGGTGTGCTCTACTTA 420

RESULT 90
BX365835 783 bp mRNA linear EST 08-APR-2004
LOCUS BX365835 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
DEFINITION BX365835
ACCESSION BX365835
VERSION BX365835
KEYWORDS BX365835.2 GI:46288859
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 783)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization.
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30370946.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdnats-CSIDB0022R030Plec=3474.r.

REFERENCE

TITLE HRI human cDNA project
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

FEATURES

1..783
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB007YB11"

/issue_type="NEUROBLASTOMA_COT_10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA_COT_10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	1,84e-45	Length:	783
Score:	439.00	Matches:	85
Percent Similarity:	98.9%	Conservative:	1
Best Local Similarity:	97.7%	Mismatches:	0
Query Match:	98.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BX365835 (1-783)

QY 1 MetGLuArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 172 ATGGAAGAGGCTTGAACCTCTGAGCCCTCCGATGAGAGAGCGCTTGGAAACG 231
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 232 CGACTGAACCATCTCTGAGCCCAACCTATKTTGACCTAACCAATGAGAAACACT 291
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 292 GATTCACACACTTCTAAATCATGAGCCATCTGAGAAATCATGAGAAATGACACACT 351
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 352 TTCTCTCATTAACCTGGAATTTGATGATTAACATCTGTCAGAGAGGCT 411
QY 81 ArgGlyValCysSerTyrLeu 87
DB 412 CGAGGGGTGTGTTCTACTTA 432

RESULT 91

CR791801

LOCUS 739 bp mRNA linear EST 01-OCT-2004

DEFINITION DKFZP468J1522.x1.468 (synonym: phr11) Pongo pygmaeus cDNA clone

CR791801

VERSION CR791801.1 GI:53710641

KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus

REFERENCE 1 (bases 1 to 739)

AUTHORS Oetjenweider,B., Obermaier,B., Deutschenbauer,S., Schaipp,A.,

Mewes,H.W., Weill,B., Amid,C., Oesanger,A., Fobo,G., Han,M. and

Wiemann,S.

TITLE Pongo pygmaeus mRNA (Oetjenweider,B., Obermaier,B.,

JOURNAL Deutschenbauer,S., et al.)

COMMENT Unpublished (2004)

CONTACT: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,

Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email: s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix

(Martinsried/Germany) within the cDNA sequencing consortium of the

German Genome Project. This clone (DKFZP468J1522) is available at

the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in

Berlin, Germany. Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/c.cgi?cloneid=DKFZP468J1522

Further information about the clone and the sequencing project is

available at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1..739

/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZP468J1522"
/issue_type="heart"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="468 (synonym: phr11)"
/note="Vector: pSPORT1_Sci; Site_1: SfilA; Site_2: SfilB"

ORIGIN

Alignment Scores:

Pred. No.:	2.3e-45	Length:	739
Score:	438.00	Matches:	85
Percent Similarity:	97.7%	Conservative:	0
Best Local Similarity:	97.7%	Mismatches:	2
Query Match:	97.8%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CR791801 (1-739)

QY 1 MetGLuArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 178 ATGGAAGAGGCTTGAACCTCTGAGCCCTCCGATGAGAGAGCGCTTGGAAACG 237
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 238 CGCCCTGAACCATCTCTGAGCCCAACCTATGTTGACCTAACCAATGAGAAACACT 297
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 298 GATTCACACACTTCTAAATCATGAGCCATCTGAGAAATCATGAGAAATGACACACT 357
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 358 TTCTCTCATTAACCTGGAATTTGATGATTAACATCTGTCAGAGAGGCT 417
QY 81 ArgGlyValCysSerTyrLeu 87
DB 418 CGAGGGGTGTGTTCTACTTA 438

RESULT 92

T26956

LOCUS 310 bp mRNA linear EST 12-JUN-1996

DEFINITION T26956 11d155proj Clontech adult human fat cell library HU1108A Homo

sapiens cDNA clone 11d155, mRNA sequence.

VERSION T26956.1 GI:575899

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 310)

AUTHORS Bouilland,F.

TITLE Study of expressed sequences tags in adipose tissue 1994

JOURNAL Unpublished (1994)

COMMENT On Nov 17, 1994 this sequence version replaced gi:624970.

Contact: Frederic Bouilland

Centre de Recherche sur l'Endocrinologie moleculaire et le

Developpement

CNRS

9, Rue Jules Hetzel, Meudon Bellevue, 92190 France

Tel: 33 1 45 07 52 87

Fax: 33 1 45 07 58 90

Email: bouilland@infobiogen.fr

Southern blot human DNA EcoRI : 2 major bands 3.1, 2.3 Kb and 2

weak : 4.2 and 1.9 Kb (wash 0.5xSSC).

Location/Qualifiers

1..310

/organism="Homo sapiens"

/mol_type="mRNA"

ORIGIN /clone_lib="Sugano cDNA library, small intestine"

Alignment Scores:

Pred. No.: 4.04e-45 Length: 580
Score: 435.00 Matches: 87
Percent Similarity: 98.9% Conservative: 0
Best Local Similarity: 98.9% Mismatches: 0
Query Match: 97.1% Indels: 1
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP261787 (1-580)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 94 ATGGAAAGGGCTGTGAACCTCTACTTCAGCCCTCCGGTGGAGAGAGCCCTTGAAACCC 153
QY 21 ATGProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 154 CCACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACACT 213
QY 41 AAPPserThrSer-LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerLeu 60
DB 214 GATTCCACCACTCTTAATATCAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCAT 273
QY 60 rheserleuilethrtipasnilleaspglyleuaspleuasnasnleusergluargal 80
DB 274 GTTCTCTCATTAACCTGGAATATGATGATTAGATCTTAACAATCTGTGAGAGGGGC 333
QY 80 aArgGlyValCySerTyrLeu 87
DB 334 TCGAGGGGTGTCTCTACTTA 355

RESULT 95

LOCUS BG119064 927 bp mRNA linear EST 30-JAN-2001
DEFINITION 602347589F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4442399 5',
mRNA sequence.

ACCESSION BG119064
VERSION BG119064.1 GI:12612570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE Homnidae; Homo.
JOURNAL 1 (bases 1 to 927)
COMMENT NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10215 row: a column: 24
High quality sequence stop: 676.

FEATURES

source 1..927
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4442399"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for

ORIGIN

full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Alignment Scores:

Pred. No.: 1.35e-44 Length: 927
Score: 433.00 Matches: 84
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 96.7% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG119064 (1-927)

QY 4 AlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArgProGlu 23
DB 1 GCTTGAACTCTCTACTTCGAGCCTCCGGTGGAGAGAGCGCTTGAAACCGCACTGAA 60
QY 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 43
DB 61 ACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAATGATCCACC 120
QY 44 ThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 63
DB 121 ACTCTTAATATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTTCTCTC 180
QY 64 lIethrtipasnilleaspglyleuaspleuasnasnleusergluargalarglyval 83
DB 181 ATTACCTGGAATATGATGATTAGATCTTAACAATCTGTGAGAGGGCTCGAGGGGTG 240
QY 84 CySerTyrLeu 87
DB 241 TGTCTCTACTTA 252

RESULT 96

LOCUS B1334820 704 bp mRNA linear EST 30-JUN-2001
DEFINITION 602998939F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141193 5',
mRNA sequence.

ACCESSION B1334820
VERSION B1334820.1 GI:15019477
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE Homnidae; Homo.
JOURNAL 1 (bases 1 to 704)
COMMENT NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11347 row: n column: 10
High quality sequence stop: 704.

FEATURES

source 1..704
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5141193"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.4 kb. Library prepared by Life Technologies."

Alignment Scores:

Pred. No.:	1.26e-44	Length:	704
Score:	432.00	Matches:	86
Percent Similarity:	98.9%	Conservative:	1
Best Local Similarity:	97.7%	Mismatches:	0
Query Match:	96.4%	Indels:	1
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) X B1334820 (1-704)

Oy	1	MeGluGAGGATATGAAAGSeTtYrPheGluGupProPoyAGluGluSeSerLAlaLeuGluArg	20
Db	147	ATGGAAAGGGCTCTGAACCTCTACTTCAGAGCTCGGGGAGAGAGCCCTTGGAAAGC	206
Oy	21	ArgProGluTrtLLeSerGluProLeuTrtYrValaIapLeuTrxAndLuuLuuTrh	40
Db	207	CGACCTGAACCACTCTGAGCCAGACCTATGTGACCTAACCAATAGAAAGAAACT	266
Oy	41	AapSerTrtTrhSerLeuLeuSerProSerGluAapTrhGluGluGluGluGluGlySerMe	60
Db	267	GATTCACCACTCTCAAAATCAGCCACTGAGAGTACTGCAAGCAAAATGCGAGAT	326
Oy	60	ePheSerLeuLLeuTrtPheLLeaPqLYLeuApuLeuApuLeuSerGluArgAl	80
Db	327	GTTCTCTTCATACCTCGGAATATGATGATTTAATGATTAACATCTCTCAAGAGGC	386
Oy	80	aArgGlyValCysSerTrpLeu	87
Db	387	TCGAGGAGGAGTGTCTTCAACTTA	406

RESULT 97	501 bp	linear	EST 14-SEP-2004
BP199948		mrna	
LOCUS			
BP199948	Sugano cDNA library,	amygdala Homo sapiens	cDNA clone
DEFINITION	AMR00446, mRNA sequence.		

REFERENCE	1 (bases 1 to 581)
AUTHORS	Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mitsushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)
PUBMED	15342556
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp.

ORIGIN		
Alignment Scores:		
Pred. No.:	1.32e-44	Length: 581
Score:	431.00	Matches: 84
Percent Similarity:	96.68	Conservative: 0

Best Local Similarity:	96.6%	Mismatches:	3
Query Match:	96.2%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) X BP199948 (1-581)

QY 1 MetGluArgAlaLeuAsnSerThr.PheGluProProValGluGluSerAlaLeuGluArg 20
Db 196 ATGAAAGAGGAGCTCTGAACCTCCTACTCGAGCTCCGGTGGAGAGAGCGCTTGAAACGC 255
QY 21 ArgProGluThrIleSerGluProGlyThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 256 GCACTGAAACCACTCTCTGAGCCCAAGACCTATGTTGACCTACCAACAGAGAAACAACCT 315
QY 41 AspSerThrThySerTyrIleSerProSerGluAspThrGluGluGluAsnGluSerMet 60
Db 316 GATTCACACACTCTTAAATATACGCCCACTCTGAAACATCTCAGCAAGAAAATGCGACATG 375
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 376 TTCCTCTCATTAACCTGGAAATATGATGATTAATCAATCTGTGAGAGAGCTC 435
QY 81 ArgGlyValCysSerTyrLeu 87
Db 436 GGGGGAGNGTGTCTTACTTA 456

	BP348796	588 bp	mrna	linear	EST 17-SEP-2004
RESULT 98					
LOCUS	BP348796				
DEFINITION	BP348796 Sugano cDNA library, brain Homo sapiens				
ACCESSION	SZRO1880, mRNA sequence.				
VERSION	BP348796				
KEYWORDS	BP348796.1 GI:52278781				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBLISHED	COMMENT
1 (Pages 1 to 588)	Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Mizushima-Sugano, J., Nakai, K. and Sugano, S.	Sequence comparison of human and mouse genes reveals block structure in the promoter regions	Genome Res. 14 (5), 1711-1718 (2004)		
	Contract	Yunaka Suzuki			
	Department of Virology				
	Institute of Medical Science, University of Tokyo				
	4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8633, Japan				
	Email: yunaka@iism.u-tokyo.ac.jp				
	Location/Qualifiers				

```

ORIGIN
/cloone_lib=Sugano cDNA library, brain"

Alignment Scores:
Fid. No.:      1.8e-44      Length:      588
Score:         430.00      Matches:     66
Percent Similarity: 98.9%   Conservative: 1
Percent Local Similarity: 97.7% Mismatches:    0
Query Match:    96.0%      Indels:      1
DB:             3          Gaps:        0

US-10-757-745-2_COPY_54_140 (1-87) x BP348796 (1-588)

Oy      1 MetGAAAGTGAATAAASerTTPheG1ProPValGIUGIUseRAlaLeuGIUAq 20
|||||

```

Db 187 ATGAAAGGGCTCTGACTCTTACTTGCAGCCTCCGGTGAGAGAGCGCTTGAGACGC 246
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 247 GCACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAACCAACT 306
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 307 GATTCACACACTCTTAAATCATGCCCATTTGAAGATCTACACAGAAATGGCAGCATG 366
QY 61 PheSerLeuIleThrTyrPheAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 367 TTCTCTCATTAACCTGGAATATGATGATTAGATCTTAACATCTGTCAAGAGGGCT 426
QY 81 Arg-GlyValCysSerTyrLeu 87
Db 427 CGAGGGGGTGTTCTCTACTTA 448
RESULT 99
BG740339 932 bp mRNA linear EST 15-MAY-2001
LOCUS BG740339
DEFINITION 602635289P1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4780318 5',
mRNA sequence.
ACCESSION BG740339 GI:14050992
VERSION BG740339
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 932)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contract: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
http://image.llnl.gov
Plate: LLM10639 row: a column: 23
High quality sequence stop: 759.
Location/Qualifiers
1..932
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4780318"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NCI;
Site 2: Salt; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.: 4,416-44 Length: 932
Score: 429.00 Matches: 83
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 95.8% Indels: 0
DB: 2 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BG740339 (1-932)
QY 5 LeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArgArgProGluThr 24
Db 3 CTGAACCTCTTACTTGAGCCTCCGGTGAGAGAGCGCTTGAGACGCCGAGCCTGAAAC 62

QY 25 IleSerGluProLysThrTyrValAspLeuThrAsnGluThrThrAspSerThrThr 44
Db 63 ATCTCTGAGCCCAACCATGATGTCCTTAACCAATGAAACCAACTGATTCACCACT 122
QY 45 SerIleSerProSerGluAspThrGlnGlnGluAsnGlySerPheSerLeuIle 64
Db 123 TCTTAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGGCAGCATGTTCTCTCAT 182
QY 65 ThrTyrPheAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCys 84
Db 183 ACCTGGAATATGATGATGATTGATTAACATCTGTCAAGAGCGCTGAGGGGTGTGT 242
QY 85 SerTyrLeu 87
Db 243 TCTTACTTA 251
RESULT 100
DQ049206 1089 bp DNA linear GSS 02-JUN-2005
LOCUS DQ049206
DEFINITION Pan troglodytes TTRAP gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ049206
VERSION DQ049206.1 GI:66902405
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
1 (bases 1 to 1089)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hudis, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civeillo, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
A scan for positively selected genes in the genomes of humans and
chimpanzees
(e) PLOS Biol. 3 (6), E170 (2005)
15869325
2 (bases 1 to 1089)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hudis, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civeillo, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
Location/Qualifiers
1..1089
source
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1089
/gene="TTRAP"
/locus_tag="HCL7203"
ORIGIN
Alignment Scores:
Pred. No.: 5,46-44 Length: 1089
Score: 429.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 3
Query Match: 95.8% Indels: 0
DB: 11 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x DQ049206 (1-1089)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 160 ATGAAAGGGCTCTGAACTCTTACTTGCAGCCTCCGGTGAGAGAGCGCTTGAGACGC 219
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40

Db 220 CGACCTGAAACATCTCTGAGCCGANNNNNNNTTGTACTTACCATGAAAGAAACAACCT 279
Qy 41 AapSerThrThSerIySllSerProSerGluapThrGlnGlnGluangIySerMet 60
Db 280 GATTCACACATCTCTAAATACGACCATCTCAAGATCTCAAGAAATATGCGACATG 339
Qy 61 PhaeSerLeuIleThrTTPanIleAapGlyLeuAapLeuAanLeuSerGluArgAla 80
Db 340 TTTCTCTCATTTACCTGGAAATATGATGATTAATGATCTAAACAATCTGTCAGAGAGGCT 399
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 400 CGAGGGGTGTGTCTACTTA 420
RESULT 101
BX422491 904 bp mRNA linear EST 03-MAY-2004
LOCUS BX422491 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM007YE11 5-PRIME, mRNA sequence.
ACCESSION BX422491
VERSION BX422491.2 GI:46955237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
AUTHORS Full-length cDNA libraries and normalization
JOURNAL On May 15, 2003 this sequence version replaced gi:30766188.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DM007AC06P1c=3474.r.
FEATURES
source location/Qualifiers
1..904
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YE11"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_1lb="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Alignment Scores:
Pred. No.: 5.68e-44 Length: 904
Score: 428.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 3
Query Match: 95.5% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BX422491 (1-904)
Qy 1 MetGluArgAlaLeuAanSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
|||||

Db 103 ATGGAAAGGCGCTCTGAATCCTTCTGAGCCTCCGATGAGAGAGCGCCTTGAAACG 162
Qy 21 ArgProGluThrIleSerGluProGlyThrTyrValAapLeuThraGlnGluThr 40
Db 163 CGACCTGAAACATCTCTGAGCCGANNNNNTTGTACTTACCATGAAAGAAACAACCT 222
Qy 41 AapSerThrThSerIySllSerProSerGluapThrGlnGlnGluangIySerMet 60
Db 223 GATTCACACATCTCTAAATACGACCATCTCAAGATCTCAAGAAATATGCGACATG 282
Qy 61 PhaeSerLeuIleThrTTPanIleAapGlyLeuAapLeuAanLeuSerGluArgAla 80
Db 283 TTTCTCTCATTTACCTGGAAATATGATGATTAATGATCTAAACAATCTGTCAGAGAGGCT 342
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 343 CGAGGGGTGTGTCTACTTA 363
RESULT 102
BP243301 556 bp mRNA linear EST 15-SEP-2004
LOCUS BP243301 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone
DEFINITION BP243301, mRNA sequence.
ACCESSION BP243301
VERSION BP243301.1 GI:52116211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
AUTHORS Mizushima-Sugano, J., Nakai, K. and Sugano, S.
JOURNAL Sequence comparison of human and mouse genes reveals a homologous
PUBMED block structure in the promoter regions
15342556 Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source location/Qualifiers
1..556
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP19431"
/tissue_type="liver"
/cell_line="HepG2"
/clone_1lb="Sugano cDNA library, liver HepG2"
/note="hepatoma"

ORIGIN
Alignment Scores:
Pred. No.: 4.04e-44 Length: 556
Score: 427.00 Matches: 83
Percent Similarity: 98.9% Conservative: 3
Best Local Similarity: 95.4% Mismatches: 1
Query Match: 95.3% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP243301 (1-556)
Qy 1 MetGluArgAlaLeuAanSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 188 ATGGAAAGGCGCTCTGAATCCTTCTGAGCCTCCGATGAGAGAGCGCCTTGAAACG 247
Qy 21 ArgProGluThrIleSerGluProGlyThrTyrValAapLeuThraGlnGluThr 40
Db 248 CGACCTGAAACATCTCTGAGCCGANNNNNTTGTACTTACCATGAAAGAAACAACCT 307
|||||

Qy 41 AepSerThrSerIleSerProSerGluAspThrGlnGluAsnGlySerMet 60
 Db 308 GATTCACACCACTTCAATCACTGATCTGAAGATCTCAGCAAGAAATGGCAGCATG 367
 Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 80
 Db 368 TTCTCATCATTAACCGAATATGATGATTAGATCTAAACATCTGTCAAGAGGGCT 427
 Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 428 CGAGAGTGTGTTCTTACTTA 448

RESULT 103
 BM172060 570 bp mRNA linear EST 04-DEC-2001
 LOCUS imagecc3_2001/sml293bdf41.xl NIH_MGC_76 Homo sapiens cDNA clone
 DEFINITION IMAGE:4700059 5', mRNA sequence.
 ACCESSION BM172060
 VERSION BM172060.1 GI:17311623
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 570)
 KALE, P.I., Harsch, T.J., Folta, P.A., Nelson, D.O., Sanders, C.G. and
 Prange, C.K.
 The I.M.A.G.E. Consortium quality control effort: clone
 resequencing for verification
 Unpublished (2001)
 Other ESTs: BG533717
 Contact: Prange CK
 The I.M.A.G.E. Consortium
 Lawrence Livermore National Laboratory
 Livermore, CA, USA
 Email: help@image.llnl.gov
 This read has been verified (found to hit its original self in the
 correct orientation), as part of the I.M.A.G.E. Consortium quality
 control effort. High quality sequence is defined as having 100 or
 more base pairs with a phred quality value of 20 or greater, where
 a sliding window of 4 base pairs with a phred quality value of 15
 or greater marks the beginning and end of the sequence. For
 information on obtaining this clone, please contact
 info@image.llnl.gov.
 Place: LLM1533 row: a column: 20
 Seq primer: -21m13
 High quality sequence stop: 570.
 Location/Qualifiers
 1..570
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4700059"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_76"
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site: 1:
 SfiI (ggcgcgcgcgcgc); Site 2: SfiI (ggccatcagcgc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCGCATATGAGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGCGCATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.85
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

Alignment Scores:
 Pred. No.: 4.17e-44 Length: 570
 Score: 427.00 Matches: 83
 Percent Similarity: 97.7% Conservative: 1
 Best Local Similarity: 96.5% Mismatches: 2

Query Match: 95.3% Indels: 0
 Db: 3 Gaps: 0
 US-10-757-745-2_COPY_54_140 (1-87) x BM172060 (1-570)

Qy 2 GUAAGTAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 21
 Db 15 CAGAGGCGCTGAACTCTTACTTCAAGCCTCCGCGAGAGAGAGCGCTTGAACGCCA 74
 Qy 22 ProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluThrThr 41
 Db 75 CCTGAACCACTCTTTATCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAATCAT 134
 Qy 42 SerThrThrSerIleSerProSerGluAspThrGlnGluAsnGlySerMetPhe 61
 Db 135 TCCACCACTTCAAAATATAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATGTTTC 194
 Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 81
 Db 195 TCTCATCATTAACCGAATATGATGATTAGATCTAAACATCTGTCAAGAGGGCTGCA 254
 Qy 82 GlyValCysSerTyrLeu 87
 Db 255 GCGGTGTGTTCTTACTTA 272

RESULT 104
 BP274942 584 bp mRNA linear EST 16-SEP-2004
 LOCUS BP274942 Sugano cDNA library, kidney Homo sapiens cDNA clone
 DEFINITION KDN02414, mRNA sequence.
 ACCESSION BP274942
 VERSION BP274942.1 GI:52188674
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 584)
 Suzuki, Y., Yamashita, R., Hirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)
 1342556
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers
 1..584
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KDN02414"
 /tissue_type="kidney"
 /clone_lib="Sugano cDNA library, kidney"

Alignment Scores:
 Pred. No.: 2.52e-43 Length: 584
 Score: 421.00 Matches: 83
 Percent Similarity: 95.4% Conservative: 0
 Best Local Similarity: 94.4% Mismatches: 4
 Query Match: 94.0% Indels: 0
 Db: 3 Gaps: 0
 US-10-757-745-2_COPY_54_140 (1-87) x BP274942 (1-584)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 Db 127 ATGGAAGAGGCTGAACTCTTCAAGCCTCCGCGAGAGAGAGCGCCTTGAACGCC 186

QY 2.1 ArgProGluThiIleSerGluProLysThrTyrValAspLeuThiAsnGluGluThiThr 40
DB 187 CGACCTGAACACCTCTGAGCCAGACCTATGTGACCTACCAATGAAAGAACAACT 246
QY 41 AAsperThiTherSerylIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGln 60
DB 247 GATTCCACACCTCTTAAATCAAGCCATCTGAGATCTGACGAAAGAAATGGCAGCATG 306
QY 61 PheSerLeuIleThiTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluAspGln 80
DB 307 TTCTCTCATTAACCTGGAATATGATGATTAATCTTAAACAATCTGCCAGAGAGGCT 366
QY 81 ArgGlyValCysSerTyrLeu 87
DB 367 CGAGGGGAGAGTACTACTTA 387
RESULT 105
BI760756 757 bp mRNA linear EST 25-SEP-2001
LOCUS 603044763F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:518534 5'
DEFINITION mRNA sequence.
ACCESSION BI760756
VERSION BI760756.1 GI:15752334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 757)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11462 row: m column: 15
High quality sequence start: 6
High quality sequence stop: 755.
Location/Qualifiers
1. 757
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:518534"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_116"
/note="Organ: Pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones. Library is constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 3.54e-43 Length: 757
Score: 421.00 Matches: 86
Percent Similarity: 98.9% Conservative: 0
Best Local Similarity: 98.9% Mismatches: 1
Query Match: 94.0% Indels: 1

DB: 3 Gaps: 0
UC-10-757-745-2_copy_54_140 (1-87) x BI760756 (1-757)
QY 1 MetGluValAlaIleAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 69 ATGGAAGAGGCTCTTAACTCTACTCTGACCTCCGATGAGGAAGAGCC-CTGAAAGCC 127
QY 21 ArgProGluThiIleSerGluProLysThrTyrValAspLeuThiAsnGluGluThiThr 40
DB 128 CGACCTGAACACCTCTGAGCCAGACCTATGTGACCTACCAATGAAAGAACAACT 187
QY 41 AAsperThiTherSerylIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGln 60
DB 188 GATTCCACACCTCTTAAATCAAGCCATCTGAGATCTGACGAAAGAAATGGCAGCATG 247
QY 61 PheSerLeuIleThiTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluAspGln 80
DB 248 TTCTCTCATTAACCTGGAATATGATGATTAATCTTAAACAATCTGCCAGAGAGGCT 307
QY 81 ArgGlyValCysSerTyrLeu 87
DB 308 CGAGGGGAGAGTACTACTTA 328
RESULT 106
BS337046 889 bp mRNA linear EST 03-APR-2001
LOCUS 602565130F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4689919 5'
DEFINITION mRNA sequence.
ACCESSION BS337046
VERSION BS337046.1 GI:13528594
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 889)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1506 row: k column: 08
High quality sequence start: 525.
Location/Qualifiers
1. 889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4689919"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH_MGC_77"
/note="Organ: Lung; Vector: pDNR-LTB (Clontech); Site 1:
SfiI (ggccctccggcc); Site 2: SfiI (ggccatctggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCGCATTTAGGCC-3' and 3' adaptor sequence:
5'-ATTCTTAGGCGCGGCGGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN
Alignment Scores:

Pred. No.: 437e-43 Length: 889
 Score: 421.00 Matches: 86
 Percent Similarity: 98.9% Conservative: 0
 Best Local Similarity: 98.9% Mismatches: 1
 Query Match: 94.0% Indels: 1
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG537046 (1-889)

QY 1 MetGUARGAlaleuanserTyrpneGluProProValGluGluSerAlaleuGUArg 20
 DB 176 ATGAAAGGGGCTGTGAACCTCTACTCGAGCCCTCGGTGAGAGAGCGCCTTGAGAGCC 235
 QY 21 ArgProGUThrlleserGluProlyThrTyrValAspLeuThraAngluThrlThr 40
 DB 236 CCACTCGAAGACCATCTCTAGCCCAAGACCTTATGTTGACCTTAACCAATGAGAAACACT 295
 QY 41 AASPserThrlserTyrpneSerProSerGluAspThrGlnGlnGluAnglySerMet 60
 DB 296 GATTCCACCACTTCTAAATCAAG-CCATCTGAAGATCTCAGCAAGAAATGCGACATG 354
 QY 61 PheSerLeuIleThrlTyrpAnlleAspGlyLeuAspLeuAsnAsnLeuSerGUArgAla 80
 DB 355 TTCTCTCTCATTAACCTGGAATATGATGATTAGATCTTAACATCTGTCAAGAGGGCT 414
 QY 81 ArgGlyValCyserTyrLeu 87
 DB 415 CGAGGGGTGTGTTCTTACTTA 435

RESULT 107

BP264149 581 bp mRNA linear EST 16-SEP-2004
 LOCUS BP264149 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION clone HS114850, mRNA sequence.
 ACCESSION BP264149
 VERSION BP264149.1 GI:52179380
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 581)
 AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556

COMMENT Contact: Yutaka Suzuki

Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source Location/Qualifiers
 1..581

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HS114850"
 /issue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"

Alignment Scores:

Pred. No.: 1.47e-42 Length: 581
 Score: 415.00 Matches: 81
 Percent Similarity: 96.5% Conservative: 2
 Best Local Similarity: 94.2% Mismatches: 0
 Query Match: 92.6% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP264149 (1-581)

QY 2 GUARGAlaleuanserTyrpneGluProProValGluGluSerAlaleuGUArg 21
 DB 129 CAGAGGGGCTGTGAACCTCTACTCGAGCCCTCGGTGAGAGAGCGCCTTGAGAGCCGA 188
 QY 22 ProGUThrlleserGluProlyThrTyrValAspLeuThraAngluThrlThr 41
 DB 189 CCGAAGACCATCTCTAGCCCAAGACCTTATGTTGACCTTAACCAATGAGAAACACTGAT 248
 QY 42 SerThrlserTyrpneSerProSerGluAspThrGlnGlnGluAnglySerMetPhe 61
 DB 249 TCACACACTTCTAAATCAAGCCCTCTGAAGATCTCAGCAAGAAATGCGACGCTTTC 308
 QY 62 SerLeuIleThrlTyrpAnlleAspGlyLeuAspLeuAsnAsnLeuSerGUArgAla 81
 DB 309 TCTCATTAACCTGGAATATGATGATTAGATCTTAACCAATCTGTCAAGAGGGCTGGG 368
 QY 82 GlyValCyserTyrLeu 87
 DB 369 GGGGTGTGTGCTGCTTG 386

RESULT 108

CN641671 1090 bp mRNA linear EST 12-MAY-2004
 LOCUS CN641671
 DEFINITION ILLUMIGEN_MCO_5159 Katze_MBR Macaca mulatta cDNA clone IB1W:5570
 5' similar to bases 11 to 990 highly similar to human TRAP
 (Hs.210628), mRNA sequence.

ACCESSION CN641671
 VERSION CN641671.1 GI:47152681
 KEYWORDS EST.
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecoinae; Macaca.

REFERENCE 1 (bases 1 to 1090)
 AUTHORS Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
 Proff, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
 Iadonato, S.P.

TITLE Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 JOURNAL Genome Biol. 6 (7), R60 (2005)
 PUBMED 15998449

COMMENT Contact: C. Magness

Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2003.12.04, 732 020 bases.

PCR Primers
 FORWARD: CCTCCTAAAGGAGCAAAA
 BACKWARD: CACTATAGCGCAATTGGTA
 Insert Length: 1090 Std Error: 0.00
 Plate: C1000043 row: E column: 07
 Seq primer: CCTCCTAAAGGAGCAAAA
 POLYA=No.

FEATURES
 source Location/Qualifiers
 1..1090

/organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IB1W:5970"
 /sex="female"
 /dev_stage="adult"
 /lab_host="E. coli SOLR"
 /clone_lib="Katze_MBR"
 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
 Site 2: Xho I; Created from StrataGene ZAP-cDNA synthesis
 kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
 Cloning Kit (catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.:	3,346-42	Length:	1090
Score:	415.00	Matches:	81
Percent Similarity:	93.1%	Conservative:	0
Best Local Similarity:	93.1%	Mismatches:	6
Query Match:	92.6%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CN61671 (1-1090)

```
OY 1 MetGUARGAlaleuanserTTPheGUPProPovaIGUIGUserAlaleuGUARG 20
DB 32 ATGAAAGCCTCTCAACCTCTCAACCTCTCAACCTCTCAACCTCTCAACCTCTCAAC 91
OY 21 AAGPUGUThThIleSerGUPProLYThTYValApleuThraAnglUGUThThr 40
DB 92 CGCCTGAAACCACTCTGAGCCCAAGACCTAGTGTGACCTAACCAATGAAAGAAACACT 151
OY 41 AAGPUGUThThIleSerGUPProSerGUPProGingGingGingGingGingGing 60
DB 152 GATTCCACCACTCTTAATATCAAGCCCAATCTGAAAGATCTACAGAAAGAAATGACAGCATG 211
OY 61 PheserleuIleThThPAsnIleAapGlyleuAapleuAanleuSerGUGUArgAla 80
DB 212 TTCTGCTTCATTAACCTGGAATATGATGATGATGATGATGATGATGATGATGATGAT 271
OY 81 ArgGlyValCyseSerTyrIleu 87
DB 272 CGAGGGGTGTGTCTTACTTA 292
```

RESULT 109

CV805216

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CV805216 827 bp mRNA linear EST 15-NOV-2004
AGENCOURT_36377305 NIH_MGC_280 Homo sapiens cDNA clone
IMAGE:7504495 5', mRNA sequence.
CV805216
CV805216.1 GI:55748182
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 827)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaspe@mail.nih.gov
Tissue Procurement: Meri Filipo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M15875 row: e column: 05
High quality sequence start: 291.
High quality sequence stop: 291.
Location/Qualifiers
1..827
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7504495"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B"
/clone_id="NIH_MGC_280"

ORIGIN

Alignment Scores:

Pred. No.:	1,832-41	Length:	827
Score:	408.00	Matches:	79
Percent Similarity:	95.3%	Conservative:	3
Best Local Similarity:	91.9%	Mismatches:	4
Query Match:	91.1%	Indels:	0
DB:	8	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CV805216 (1-827)

```
OY 1 MetGUARGAlaleuanserTTPheGUPProPovaIGUIGUserAlaleuGUARG 20
DB 194 ATGAAAGCCTCTCAACCTCTCAACCTCTCAACCTCTCAACCTCTCAACCTCTCAAC 253
OY 21 AAGPUGUThThIleSerGUPProLYThTYValApleuThraAnglUGUThThr 40
DB 254 CGACCTGAAACCACTCTGAGCCCAAGACCTAGTGTGACCTAACCAATGAAAGAAACACT 313
OY 41 AAGPUGUThThIleSerGUPProSerGUPProGingGingGingGingGingGing 60
DB 314 GATTCACCACTCTCAATATCAAGCCCAATCTGAAAGATCTACAGAAAGAAATGCGCATG 373
OY 61 PheserleuIleThThPAsnIleAapGlyleuAapleuAanleuSerGUGUArgAla 80
DB 374 TTCTGCTTCATTAACCTGGAATATGATGATGATGATGATGATGATGATGATGATGAT 433
OY 81 ArgGlyValCyseSerTyr 86
DB 434 CGAGGGGTGTGTCTTACTTA 451
```

RESULT 110

B1915865

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B1915865 915 bp mRNA linear EST 16-OCT-2001
603184527F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248495 5',
mRNA sequence.
B1915865
B1915865.1 GI:16179808
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 915)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaspe@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1AM1627 row: e column: 08
High quality sequence stop: 696.
Location/Qualifiers

FEATURES

Source

1..915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5248495"
/lab_host="DH10B"
/clone_11b="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 4,36e-41 Length: 915
Score: 405.50 Matches: 83
Percent Similarity: 95.5% Conservative: 2
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 90.5% Indels: 2
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x B1915865 (1-915)

QY 1 MetGUAAGAlaLeuAnsSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 167 ATGGAAGGGCTCTGAACCTCTGAGCTCCGGTGGAGAGAGCGCTTGGAAAGC 226

QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
DB 227 CGACCTGAAACCACTCTGAGCCCAAGACCTAGTGGACTTAACAATGAAGAAACACT 286

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 287 GATTCACACCACTTCAAAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGGCAGCAG 346

QY 61 PheSerLeuIleThrTrpAsnIleAsp-GlyLeuAspLeuAsnLeuSer---GluArg 79
DB 347 TTCTCTCATTAACCTCGAATATGATCGATTAGATCTTAACAATCTCTCAGACGAGG 406

QY 79 GAlaArgGlyValCySerTyRLeu 87
DB 407 CTCGACGGGGCTGTGTTCTCTACTTA 431

RESULT 111

BQ787387

LOCUS BQ787387 352 bp mRNA linear EST 26-JUL-2002

DEFINITION 5' similar to TR:095551 095551 D330M3.3 ; mRNA sequence.

ACCESSION BQ787387

VERSION BQ787387.1 GI:21995859

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 352)

Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,

Lemisha, I., Pearce, M., Brestelli, J., Gradow, G., Clifton, R.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistein, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R.,

Williams, T., Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

JOURNAL COMMENT

Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to

pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a

clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)

Seq primer: 40RP from Gibco.

Location/Qualifiers

1..352

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:603453"

/tissue_type="Insulinoma"

/lab_host="DH10B (phage-resistant)"

/clone_11b="Human insulinoma"

/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:

XhoI; Site 2: EcoRI; Constructed with lambda ZAPIT system

(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to

pBluescript SK- by Dr. H. Inoue following the Washington

University protocol

(http://genome.wustl.edu/est/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further

information on this library (Metabolism Division, Permut

Laboratory, Washington University School of Medicine, Box

8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this

is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.: 1.45e-41 Length: 352
Score: 405.00 Matches: 79
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.4% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BQ787387 (1-352)

QY 1 MetGUAAGAlaLeuAnsSerTyRphGluProProValGluGluSerAlaLeuGluArg 20

DB 115 ATGGAAGGGCTCTGAACCTCTGAGCTCCGGTGGAGAGAGCGCTTGGAAAGC 174

QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40

DB 175 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACAATGAAGAAACACT 234

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

DB 235 GATTCACACCACTTCAAAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGGCAGCAG 294

QY 61 PheSerLeuIleThrTrpAsnIleAsp-GlyLeuAspLeuAsnLeuSerGluArg 79

DB 295 TTCTCTCATTAACCTCGAATATGATCGATTAGATCTTAACAATCTCTCAGACGAG 351

RESULT 112

CN801806

LOCUS CN801806 922 bp mRNA linear EST 26-MAY-2004

DEFINITION ILLUMIGEN MCQ 37066 Kacz MBR Macaca mulatta cDNA clone

IB1UP:15450 5' similar to Bases 18 to 922 highly similar to human

TRAP (Hs:210628), mRNA sequence.

ACCESSION CN801806

VERSION CN801806.1 GI:47697782

KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.
1 (bases 1 to 922)
Magnes, C.L., Felling, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
1599449
Contact: C. Magnes
illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnes@illumigen.com
Sequenced on 2004.05.13. 514 Q20 bases.
PCR primers
FORWARD: CCTCACTAAAGGACAAACAAA
BACKWARD: CACTATAGGCGAATTGGGTA
Insert Length: 922 Std Error: 0.00
Plate: C0000291 row: H column: 09
Seq primer: CCTCACTAAAGGACAAACAAA
POLYA=No

FEATURES

source

Location/Qualifiers

1..922
/mol_type="Macaca mulatta"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUM.15450"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze, MMBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site: 1; Ecor I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
Kit (catalog #200400) and ZAP-cDNA GigaPack III Gold
Cloning Kit (catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.:	1,660-40	Length:	922
Score:	401.00	Matches:	80
Percent Similarity:	33.1%	Conservative:	1
Best Local Similarity:	92.0%	Mismatches:	6
Query Match:	89.5%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CN801806 (1-922)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluGluSerAlaLeuGluArg 20
DB 42 ATGACACAGGCTCTGATCTCTGATTCGAGCTCCGCTGAGAGAGCCGCTTGAAGC 101
QY 21 ArgProGluThrIleSerGluProProValArgValAspLeuThrAsnGluGluThr 40
DB 102 CCGCTTAACCACTCTGAGCCCAAGACCTATGTTACCTAACCAATGAGAACT 161
QY 41 AspSerThrThrSerValIleSerProSerGluAspThrGluGluGluSerMet 60
DB 162 GATTCACCACTCTTAAATCTAGCCCATCTGAGATCTCGACAGAAATGACAGC 221
QY 61 PheSerLeuIleThrTyrPheIleAspGluLeuAspLeuAsnLeuSerGluArgAla 80
DB 222 TTCGCTTCATTTACCTGAGATTTGATGATTAATCTAAACATCTGTACAGAGCGCT 281
QY 81 ArgGluValCysSerTyrIleu 87
DB 282 CAGGAGGTGTCTCTACTTA 302
RESULT 113

BU070378/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU070378 347 bp mRNA linear EST 27-AUG-2002
IM09C09.x1 Human Insulinoma Homo sapiens cDNA clone IMAGE:6034553
3' similar to IR:095551 O95551 DJ30M3.3 ; mRNA sequence.
BU070378.1 GI:22511567
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 347)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Glickson, S.,
Hillier, L., Maira, M., Pape, D., Wylie, T., Martin, V., Biletain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, V.,
Cardenas, M., Gibbons, M., McCam, R., Cole, R., Tsagaris, V., R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: IM09C09.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biomph.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pInuScript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.

FEATURES

source

Location/Qualifiers

1..347
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6034553"
/issue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/note="Organ: pancreas; Vector: pInuScript SK-; Site: 1;
XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pInuScript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/ast/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.:	6,196-41	Length:	347
Score:	400.00	Matches:	78
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	89.3%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BU070378 (1-347)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluGluSerAlaLeuGluArg 20
DB 234 ATGAAAAGGCTCTGAACTCTCAAGCTCCGCTGAGAGAGAGCCCTTGAAGC 175
QY 21 ArgProGluThrIleSerGluProProValArgValAspLeuThrAsnGluGluThr 40

QY 20 GATGPGGGLU-THrIleSeRGLUp-roLyThrTYrValAsePLeu--THrAnGIuGIuTh 39
 DB 219 CGACCTGTAACCACTCTGAGCCCAAGACCTTGTGACTGACCAAGAGAAAC 278
 QY 39 rThrASeRThrThrSeLyIleSeRProSeGluASePThGInGInGluAAGlySe 59
 DB 279 AACTGATTCACACCTCTTAATATGACCCCTGAGATCTCAGCAAGAAATGGCAG 338
 QY 59 rMetPheSeRLeuIleThrTPAnIleASeGlyLeuASePLeuASeRLeuSeuGlyA 79
 DB 339 CATGTCCTCTCATTAACCTGGAATATGATGATGATCTTAACCAATCTGTCAAGAG 398
 QY 79 GAlAaRGlyValCySeSeTYrLeu 87
 DB 399 GGCCTGAGGGGGTGTGTTCTTACTTA 423

RESULT 116

BG391295 770 bp mRNA linear EST 12-MAR-2001
 LOCUS 60241734efl NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4536634 5'
 DEFINITION mRNA sequence.
 ACCESSION BG391295
 VERSION BG391295.1 GI:13284743
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: sgaps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LHAM10460 row: h column: 11
 High quality sequence stop: 693.

FEATURES

source

1..770
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4536634"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site: 1; NCI; Site: 2; Salt; Cloned unidirectionally; Oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 2.63e-38 Length: 770
 Score: 383.00 Matches: 84
 Percent Similarity: 93.4% Conservative: 1
 Best Local Similarity: 92.3% Mismatches: 2
 Query Match: 85.5% Indels: 4
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG391295 (1-770)

QY 1 MetGluArgAlaLeuAuaSerTYrPheGluProPro-ValGluGluSerAlaLeuGluAr 20
 DB 167 ATGGAAGGGCTGGAATCTCTACTTCGAGCCTCCGTGTGAGAGAGAGAGCCCTTGGAGG 226

QY 20 GATGPGGGLUThrIleSeRGLUp-roLyThrTYrValAsePLeuThrAnGIuGIuThrTh 40
 DB 227 CGACCTGTAACCACTCTGAGCCCAAGACCTTGTGACTGACCAATGAGAAACAGC 286
 QY 40 rASeRThrThrSeLyIleSeR-ProSeGluASePThGInGInGluAAGly-Seq 59
 DB 287 TGAATTCACACCTCTTAATATGATGATGATGATCTTAACCAATCTGTCAAGAG 346
 QY 60 MetPheSeRLeuIleThrTPAnIleASeGlyLeuASePLeuASeRLeuSeuGlyA 79
 DB 347 ATGTCCTCTCATTAACCTGGAATATGATGATGATCTTAACCAATCTGTCAAGAG 406
 QY 79 GAlAaRGlyValCySeSeTYrLeu 87
 DB 407 GGCCTGAGGGGGTGTGTTCTTACTTA 431

RESULT 117

BH507091 582 bp mRNA linear EST 15-FEB-2002
 LOCUS 1124201.y1 Human insulinoma Homo sapiens cDNA 5' similar to
 DEFINITION TR:095551 095551 DJ30M2.3 ?, mRNA sequence.
 ACCESSION BH507091
 VERSION BH507091.1 GI:18678234
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 582)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Scaerle, M., Brecht, J., Gradow, G., Clifton, S.,
 Hillier, L., Karia, M., Pape, D., Wylie, R., Martin, J., Bliscorn, A.,
 Schmitz, A., Theising, B., Kletter, B., Komko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McGann, R., Cole, R., Teagarden, J., R.,
 Williams, T., Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: 1124201.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Harvard University, Howard Hughes Medical Institute
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmellon@biochem.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue DNA sequencing by Washington
 University Genome Sequencing Center for information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 269.

FEATURES

source

1..582
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Human insulinoma"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site: 1;
 XhoI; Site: 2; EcoRI; Constructed with lambda ZAPIT system
 (Stratagene) by Dr. J. Ferrer in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further
 laboratory on this library (Metabolism Division, Permutt
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas EST project library."

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.isrt

Page 68

US-10-757-745-2_COPY_54_140 (1-87) x AL516230 (1-816)

OY 2 GUUAGAlaleuanserTyrPheGluProProValGluGluSerAlaLeuGluuArg-AR 21
DB 194 GAAAGGGCTCTAAGCTTCTAGACCTCCGCTGAGAGAGAGCGCTTGGAACGCGCG 253
OY 21 GPROGUTNriIeserGluProLystrTyrValaApleuTrnaAngluGluTrnaA 41
DB 254 ACCTGAACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACACCTGA 313
OY 41 PserTrnTrserTysIleserProserGluAapTrn--GlnGlnGluAangIyser-Me 60
DB 314 TTCACCACTTCTAAATCAGCCATCTGAGATAGCTCAGCAAGAAATGGCAGCGAT 373
OY 60 CpneserleuIletrn-TTpaenIleapGlyleuAap'euansnleuSerGluArg 80
DB 374 GTKCTCTCATTAAGCTGGAATATTGATGATTAAGTCAAAACATCTGTCAAGAGGG 433
OY 80 laArgIyValCysserTyrleu 87
DB 434 CTCAGGGGTGTCTKCTACTTA 456

RESULT 120

LOCUS AV61333 394 bp mRNA linear EST 16-JAN-2002
DEFINITION AV61333 GLC Homo sapiens cDNA clone GICGRD01 3', mRNA sequence.
ACCESSION AV61333
VERSION AV61333.1 GI:9882347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL

PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source
1..394
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GICGRD01"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_idb="GLC"
/note="Vector: pBluescript SK(-), Site_1: EcoRI, Site_2:
XhoI"

ORIGIN

Alignment Scores:
Pred. No.: 2,31e-35 Length: 394
Score: 357.00 Matches: 69
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 79.7% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AV61333 (1-394)

OY 19 GUUAGARGProGluTrnriIeserGluProLystrTyrValaApleuTrnaAngluGlu 38
DB 2 GAAGCCAGACCTGAACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAA 61
OY 39 TTTTAApSerTrnTrserTysIleserProserGluAapTrnGlnGlnGluAangI 58
DB 62 ACACCTGATTCACCACTTCTAAATCAGCCATCTGAGATAGCTCAGCAAGAAATGGC 121
OY 59 SerMetPheSerleuIletrn-TTpaenIleapGlyleuAap'euansnleuSerGlu 78
DB 122 AGCATGTTCTCTCATTAAGCTGGAATATTGATGATTAAGTCAAAACATCTGTCAAG 181
OY 79 ArgAlaArgIyValCysserTyrleu 87
DB 182 AGGGCTCGAGGGGTGTCTCTACTTA 208

RESULT 121

LOCUS T31666 325 bp mRNA linear EST 06-SEP-1995
DEFINITION EST316732 Human Embryo Homo sapiens cDNA 5' end similar to None,
mRNA sequence.
ACCESSION T31666
VERSION T31666.1 GI:613764
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Adams,M.D., Kertlavage,A.R., Fleischmann,R.D., Pulner,R.A.,
Balt,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chui,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Barle-Hughes,J., Fite,L.D.,
Flitzgerald,L.M., FlitzHugh,W.M., Fritchman,J.L., Georgiagen,N.S.M.,
Gjodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,P.S.,
Killey,J.M., Klinek,K.M., Kelley,J.C., Liu,J.-I., Matmaros,S.M.,
Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T.,
Pallergino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utebeck,T.R.,
Weidman,J.F., Li,Y., Bedarid,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,B.-J., Dinke,D., Feng,P., Ferris,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,D., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Li,H., Li,H.,
Matsner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wang,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseitine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)

JOURNAL

PUBMED 7566098
COMMENT Contact: Venter, JC
The Institute for Genomic Research
932 Clapper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse
Location/Qualifiers
1..325
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (Inhost):101908"
/db_xref="taxon:9606"
/tissue_type="embryo"
/clone_idb="Human Embryo"

FEATURES

source
ORIGIN

Alignment Scores:

Pred. No.: 4,84e-33 Length: 325
 Score: 338.00 Matches: 68
 Percent Similarity: 98.6% Conservative: 1
 Best Local Similarity: 97.1% Mismatches: 0
 Query Match: 75.4% Indels: 1
 DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x T31666 (1-325)

QY 1 MetGUARGAlaleuanserTyrPhegluPProProValGluGluSerAlaleuGuarg 20
 DB 116 ATGGAAGAGGGCTCTGAACTCTTCACTTCCAGCTCCGCTGAGAGAGAGCCCTTGAAACC 175
 QY 21 ArgProgluThrIleSerGluProlyThrTyrValAspLeuThrAsnGluGluThr 40
 DB 176 CGACCTGAACCATCTCTAAGCCCAAGACCTAAGTGAACCTAACCAATGAGAAACAAC 235
 QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 236 GATTCACACACTTCTAAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGCGACATG 295
 QY 61 PheSerLeuIleThrTyrAsnIleAsp 69
 DB 296 TTCTCTCTAATTAACCTGGAATTTGAT 323

RESULT 122

LOCUS CN791432 674 bp mRNA linear EST 26-MAY-2004
 DEFINITION 4126159 BARC 8BOV Bos taurus cDNA clone 8BOV_42E11 5', mRNA
 sequence.
 ACCESSION CN791432
 VERSION CN791432.1 GI:47687412
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 674)
 Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
 Matukumalli,L.K.

TITLE

Construction and Analysis of a cDNA Library Generated From
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle
 Unpublished (2004)

JOURNAL COMMENT
 Contact: Richard G. Baumann
 Bovine Functional Genomics Lab
 ANRI

Bldg 162; BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim alt '' -trim fasta. Vector identified
 by cross match using options -mismatch 12 -minscore 18
 Plate: 42 Row: B Column: 11
 Seq primer: CCTATTAGGTGACACTATAGAAC
 High quality sequence stop: 674.
 Location/Qualifiers

FEATURES

1..674
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_42E11"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stage="Lactating, Neonatal"
 /lab_host="DH10B TONa"
 /clone_11b="BARC 8BOV"
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site_1:
 Note1, Site_2: EcorI; Normalized cow cDNA intestinal

ORIGIN

library in pCMVSPORT6.1, constructed from equimolar mRNA
 pools derived from 5 sources, 4 lactating intestinal, 1
 neonatal intestinal 4/5 lactating, proximal duodenum,
 jejunum, distal ileum, colon, 1/5 Neonatal, proximal
 duodenum, jejunum, distal ileum"

Alignment Scores:

Pred. No.: 9,89e-32 Length: 674
 Score: 331.00 Matches: 67
 Percent Similarity: 83.1% Conservative: 7
 Best Local Similarity: 75.3% Mismatches: 13
 Query Match: 73.9% Indels: 2
 DB: 7 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x CN791432 (1-674)

QY 1 MetGUARGAlaleuanserTyrPhegluPProProValGluGluSerAlaleuGuarg 20
 DB 61 ATGGAAGAGGGCTCTGAACTCTTCACTTCCAGCTCCGCTGAGAGAGAGCCCTTGAAACC 120
 QY 21 ArgProgluThrIleSerGluProlyThrTyrValAspLeuThrAsnGluGluThr 40
 DB 121 CGTCCGAGTCCCTCTGAGCTCGGTCTGTGACCTAACCAAGAAACAAT 180
 QY 41 AspSerThrThrSerIleSerProSerGluAsp-----ThGlnGlnGluAsnGly 58
 DB 181 GATTCATTAATCTTCTAAACCAACCATCTGAAGATCAATGTTCAAGCAAGATGCGC 240
 QY 59 SerMetPheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnIleSerGlu 78
 DB 241 AGTGAATCTCTTTCATTAACCTGGAATTTGATGATGATGATGATGATGATGATGATGAT 300
 QY 79 ArgAlaArgGlyValCysSerTyrIleu 87
 DB 301 AGGCTCGAGGGGGTGTGTTCCATTTA 327

RESULT 123

LOCUS AV659558 388 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV659558 GLC Homo sapiens cDNA clone GLCFYD04 3', mRNA sequence.
 ACCESSION AV659558
 VERSION AV659558.1 GI:9880572
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo
 1 (bases 1 to 388)
 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z. and Han,Z.

REFERENCE

Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

TITLE

Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

JOURNAL

PUBMED
 11752456
 Contact: Zenguan Han

Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

1..388
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GLCFYD04"

/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="c1t1"
/lab_host="SCLR"
/clone_id="GIC"
/note="Vector: pBluescript sk(-), Site_1: EcoRI, Site_2:
XhoI"

ORIGIN

Alignment Scores:
Pred. No.: 8,65e-32 Length: 388
Score: 329.00 Matches: 68
Percent Similarity: 79.3% Conservative: 1
Best Local Similarity: 78.2% Mismatches: 0
Query Match: 73.4% Indels: 18
DB: 1 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x AV659558 (1-388)

OY 1 MetGluArgAlaLeuAnsSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 96 ATGAAAGGGCTCTGAACCTCTGAGCTCCGCTGAGAGAGAGCGCTTGAACGC 155
OY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 156 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTCACCTAACCAATGAAGAAACAAC 215
OY 41 AspSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 216 GATTCCACCACTTCAATATCAGCCCACTGAGAGATCTCAGCAAGAC----- 263
OY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 264 -----AATCTGTCAAGAGGGCT 281
OY 81 ArgGlyValCysSerTyrLeu 87
DB 282 CGAGGGGTGTGTTCTACTTA 302

RESULT 124
BP349936 581 bp mRNA linear EST 17-SEP-2004
LOCUS BP349936 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION SZR06923, mRNA sequence.
ACCESSION BP349936
VERSION BP349936.1 GI:52279921
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 581)
Susuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED

CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SZR06923"
/tissue_type="brain"
/clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:

Pred. No.: 1,47e-31 Length: 581
Score: 329.00 Matches: 64
Percent Similarity: 98.5% Conservative: 0
Best Local Similarity: 98.5% Mismatches: 1
Query Match: 73.4% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP349936 (1-581)

OY 23 GluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAspSer 42
DB 3 GAAACCATCTTGAGCCCAANACCTATGTTGACCTTAACCAATGAAGAAACAACGATTC 62
OY 43 ThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSer 62
DB 63 ACCACTTCTTAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTTCTCT 122
OY 63 LeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGly 82
DB 123 CTCATTACCTGGAATATGATGATTAATCAATCAATCTGTGAGAGAGGCTCGAGGG 182
OY 83 ValCysSerTyrLeu 87
DB 183 GTGTGTCTCACTTA 197

RESULT 125
CF788416 467 bp mRNA linear EST 21-OCT-2003
LOCUS CF788416
DEFINITION 860384 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CF788416
VERSION CF788416.1 GI:37792977
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;

REFERENCE 1 (bases 1 to 467)
Smith, T.F., Fekling, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Kohnman, D.J., May, J.E. and Keale, J.W.
Single pass sequencing. Bases called with phred v0.020425.c and
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2002)
CONTACT: Smith TF
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_aln option. Vector identified with
cross_match v0.990329.
Seq primer: TMM8003 row: J column: 8
Plat primer: GMAATCGACTCATATGAGG.
Location/Qualifiers
1..467
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9623"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P1G"
/note="Vector: pCDNA3.1, Site_1: EcoRI, Site_2: NotI;
library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

FEATURES

source
1..467
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9623"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P1G"
/note="Vector: pCDNA3.1, Site_1: EcoRI, Site_2: NotI;
library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:
Pred. No.: 1.99e-31 Length: 467
Score: 327.00 Matches: 64
Percent Similarity: 86.2% Mismatches: 11
Best Local Similarity: 73.6% Gaps: 12

Query Match:

73.0%

Indels: 0

Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CF788416 (1-467)

QY 1 MetGUAGAGAlaLeuAnserTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 179 ATGAAAGAGCCCTGAACTCTTCTCGAGCCGCGGTGAGAGAAAGCCCTTTAAAGT 238
 QY 21 ArgProGluThrIleSerGluProValTyrValAspLeuThrAngGluGluThr 40
 DB 239 CCTCTGAGAGACCCCAATGAGCCGAGTCTGTGTGACTTAACCAAGAGAAACAAGT 298
 QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAnGIysMet 60
 DB 299 GATTCCTTAGTGTGTAACCAAGACATCTGAAATGTTTCAGCAAGAAAGATGCGAGTGTG 358
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAnLeuSerGluArgAla 80
 DB 359 TTCTCTTCATTAACCTGGAATATGATGATGAGACTTAACAGTCTGCTCGAGAGGGCT 418
 QY 81 ArgGlyValCysSerTyrIleu 87
 DB 419 CGAGGGGTGTGTTCTATTTA 439

RESULT 126

LOCUS DN122208 798 bp mRNA linear EST 15-FEB-2005
 DEFINITION 1122397 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION DN122208
 VERSION DN122208.1 GI:59816487
 KEYWORDS EST
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 798)
 AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
 Nonneman,D.J., Wray,J.E. and Keele,J.W.
 TITLE Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 JOURNAL Unpublished (2003)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alit option. Vector identified with
 cross_match v0.990329.
 Plate: HHY8024 row: L column: 17
 Seq primer: GTAATGACCTCACTATAGGG.
 Location/Qualifiers
 1..798

FEATURES

source
 1..798
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4P1G"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:

Pred. No.: 4.01e-31 Length: 798
 Score: 327.00 Matches: 64
 Percent Similarity: 86.2% Conservative: 11
 Best Local Similarity: 73.6% Mismatches: 12
 Query Match: 73.0% Indels: 0

DB:

8

Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x DN122208 (1-798)

QY 1 MetGUAGAGAlaLeuAnserTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 180 ATGAAAGAGCCCTGAACTCTTCTCGAGCCGCGGTGAGAGAAAGCCCTTTAAAGT 239
 QY 21 ArgProGluThrIleSerGluProValTyrValAspLeuThrAngGluGluThr 40
 DB 240 CCTCTGAGAGACCCCAATGAGCCGAGTCTGTGTGACTTAACCAAGAGAAACAAGT 299
 QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAnGIysMet 60
 DB 300 GATTCCTTAGTGTGTAACCAAGACATCTGAAATGTTTCAGCAAGAAAGATGCGAGTGTG 359
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAnLeuSerGluArgAla 80
 DB 360 TTCTCTTCATTAACCTGGAATATGATGATGAGACTTAACAGTCTGCTCGAGAGGGCT 419
 QY 81 ArgGlyValCysSerTyrIleu 87
 DB 420 CGAGGGGTGTGTTCTATTTA 440

RESULT 127

LOCUS CF764797 648 bp mRNA linear EST 17-OCT-2003
 DEFINITION CF764797
 ACCESSION CF764797
 VERSION CF764797.1 GI:37714016
 KEYWORDS EST
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 648)
 AUTHORS Wang,Y.H., McWilliam,S. and Lehnert,S.
 TITLE Transcription profiling of cattle skin
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dr Yonhong Wang
 Functional Genomics Lab
 CSIRO Livestock Industries
 Level 5, Queensland Biosciences Precinct, University of Queensland,
 306 Carmody Road St. Lucia QLD Australia
 Tel: 07 3214 2445
 Fax: 07 3214 2685
 Email: Yonhong.Wang@csiro.au
 Plate: 41 row: G column: 05.
 Location/Qualifiers
 1..648

FEATURES

source
 1..648
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Hereford Shorthorn"
 /db_xref="taxon:9913"
 /clone="CCF003181"
 /sex="female"
 /tissue_type="pooled"
 /dev_stage="Adult"
 /lab_host="XLI-BlueMRF strain"
 /clone_lib="Bos taurus skin cDNA library"
 /note="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcoRI;
 Site 2: Xho I; library made from pooled skin of adult
 female Hereford-Shorthorn."

ORIGIN

Alignment Scores:

Pred. No.: 5.5e-31 Length: 648
 Score: 325.00 Matches: 66
 Percent Similarity: 82.0% Conservative: 7
 Best Local Similarity: 74.2% Mismatches: 14
 Query Match: 72.5% Indels: 2

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.rst

Page 72

DB: 6 Gaps: 1
US-10-757-745-2_COPY_54_140 (1-87) x CF764797 (1-648)

OY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 68 ATGAAAGAGCCCTAACTCTGACCCGCGCGAGAGAGAGCGCTTCAGAAAGC 127
OY 21 ArgProGluThrIleSerGluProLeuTyrValAspLeuThrAsnGluThrThr 40
DB 128 CGTCCGAGTCCCTCTGAGCCGCGCTCTGTGTGACCTAACCAAGAAACAAAT 187
OY 41 AspSerThrThrSerIleIleSerProSerGluAsp-----ThrGlnGlnGluAsnGly 58
DB 188 GATTCATTAGTCTTAAACCAACGACATCTGAGAGATAAAAGTGTTCAGCAAGAAAGATGC 247
OY 59 SerMetPheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGlu 78
DB 248 AGTGTATGTCCTTCTTACCTGAGATATGATGATGACATGAAACATCTCTAGAG 307
OY 79 ArgAlaArgGlyValCysSerTyrLeu 87
DB 308 AGGCTCGAGGGGTGTGTTCTATTTA 334

RESULT 128

CN789157 683 bp mRNA linear EST 26-MAY-2004
LOCUS 4123581 BARC 8BOV Bos taurus cDNA clone 8BOV_37N03 5', mRNA
DEFINITION

ACCESSION CN789157
VERSION CN789157
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
AUTHORS 1 (bases 1 to 683)
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
Metukumalli,L.K.
TITLE Construction and Analysis of a cDNA Library Generated from
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt '-trim fasta. Vector identified
by cross match using options -mismatch 12 -minscore 18
Plate: 37 row: N column: 03
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 683.
Location/Qualifiers

FEATURES

source 1..683
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV_37N03"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TONa"
/clone_id="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site: 1;
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,

ORIGIN

Alignment Scores:
Pred. No.: 5.89e-31 Length: 683
Score: 325.00 Matches: 56
Percent Similarity: 82.0% Conservative: 14
Best Local Similarity: 74.2% Mismatches: 2
Query Match: 72.5% Indels: 1
DB: 7 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x CN789157 (1-683)

OY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 55 ATGAAAGAGCCCTAACTCTGACCCGCGCGAGAGAGAGCGCTTCAGAAAGC 114
OY 21 ArgProGluThrIleSerGluProLeuTyrValAspLeuThrAsnGluThrThr 40
DB 115 CGTCCGAGTCCCTCTGAGCCGCGCTCTGTGTGACCTAACCAAGAAACAAAT 174
OY 41 AspSerThrThrSerIleIleSerProSerGluAsp-----ThrGlnGlnGluAsnGly 58
DB 175 GATTCATTAGTCTTAAACCAACGACATCTGAGAGATAAAAGTGTTCAGCAAGAAAGATGC 234
OY 59 SerMetPheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGlu 78
DB 235 AGTGTATGTCCTTCTTACCTGAGATATGATGATGACATGAAACATCTCTAGAG 294
OY 79 ArgAlaArgGlyValCysSerTyrLeu 87
DB 295 AGGCTCGAGGGGTGTGTTCTATTTA 321

RESULT 129

B1181461 750 bp mRNA linear EST 10-JUL-2001
LOCUS UNL-P-FN-ak-a-12-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
DEFINITION

ACCESSION B1181461
VERSION B1181461
KEYWORDS UNL-P-FN-ak-a-12-0-UNL.s1 mRNA sequence.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 750)
Caetano,A.R., Johnson,R.K. and Pomp,D.
AUTHORS Generation and sequence characterization of a normalized cDNA
TITLE library from swine ovarian follicles
JOURNAL Mamm. Genome 14 (1), 65-70 (2003)
PUBMED 12532269
COMMENT Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dt crack not found, Not I site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
POLYA=No.

FEATURES

source 1..750
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="University of Nebraska, Lincoln Swine Selection
Lines"
/db_xref="taxon:9923"
/clone="UNL-P-FN-ak-a-12-0-UNL"
/dev_stage="ADULT"

/lab_host=DDH08 (Life Technologies)"
 /clone_lib="UNL-P-FN"
 /notes=Vector: .pP73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UNL-P-FN
 library is a normalized library representing porcine
 ovarian follicles, ranging between 2.0 to 10.0 mm in
 diameter, collected during 7 days of the follicular phase
 of the pig estrous cycle. This library was derived from
 the library UNL-P-F2. The tag is a string of 5-6
 nucleotides present between the Not I site and the
 oligo-dT track. The library was constructed as described
 by Bonaldo, Lemon and Soares, Genome Research 6 :
 791-806, 1996.
 TAG_SEQ=None found"

The following treatments: 1) no treatment; 2) *Salmonella choleraesuis* vaccine strain SC-54; 3) phorbol myristate acetate, concanavalin A, and 8-bromo-cyclic AMP; and 4) lipopolysaccharide and cholera toxin. Each treatment was performed in the presence and absence of cycloheximide. Purified poly A⁺ RNA from each of the treated tissues (2-4) was combined together, reverse transcribed, and cloned in to pCMVSPORT6 to make a library of approximately 530,000 recombinant clones with an average insert size of 1.0 kbp. Poly A⁺ RNA from freshly isolated and non-treated tissue from an Ussing chamber (treatment 1) was cloned in the same manner to produce an unstimulated cDNA library of approximately 900,000 clones with an average insert size of 1.5 kbp. Equal portions of the two libraries were pooled and then subtracted with porcine ST fibroblast RNA to create a subtracted porcine Peyer's patch library of approximately 6,000 clones with an average insert size of 1.0 kbp."

ORIGIN

Alignment Scores:	
Pred. No.:	2.19e-29
Score:	312.00
Percent Similarity:	85.7%
Best Local Similarity:	72.6%
Query Match:	69.6%
DB:	6
	Gaps:
	0

QY	4	AlaLeuAsnSerLy ¹ Pro ¹ He ¹ u ¹ Pro ¹ Val ¹ Gl ¹ u ¹ u ¹ Ser ¹ Ala ¹ Leu ¹ u ¹ Arg ¹ Arg ¹ Pro ¹ Gl ¹ u ¹ 23
	
Db	1	GGCTGAACCTCACTTCAGCGCGGCGGTGAGGAGAAAGCTTTAAAAAGTCGCTCGAG60
QY	24	Thr ¹ IleSer ¹ Gl ¹ u ¹ Pro ¹ Ly ¹ Thr ¹ Tyr ¹ Val ¹ Asp ¹ Leu ¹ Thr ¹ Asn ¹ Gl ¹ u ¹ u ¹ Thr ¹ Thr ¹ Asp ¹ Thr ¹ 43
	
Db	61	ACCCCAAGAGGCCCAAGTCCTGTGTGACTTAAACCAAGAAAGAAACAAGATTCCTTT120
QY	44	ThrSerLy ¹ IleSerProSerGl ¹ u ¹ Asp ¹ Thr ¹ Gln ¹ Gln ¹ u ¹ Asn ¹ Ly ¹ SerMetPheSerLeu63
	
Db	121	AGTGTGAAAAACGACGACATCTGAABAATGTTCACGAAGAAGATGGCAGTGCTCTCTTTC180
QY	64	IleThr ¹ TyrAsn ¹ IleAsp ¹ Ly ¹ Leu ¹ Asp ¹ Leu ¹ Asn ¹ Leu ¹ Ser ¹ Gl ¹ u ¹ Arg ¹ Ala ¹ Arg ¹ Val ¹ 83
	
Db	181	ATTACCTGGAAATATAGATGATTTGGAACCTAAAGCTCTGCTCGAGAGGGCTCGAGGGGTG240
QY	84	CysSer ¹ TyrLeu87
	
Db	241	TGTTCTCATTTTA252

RESULT 133	
LOCUS	BP270589
DEFINITION	BP270589 Sugano cDNA library, small intestine Homo sapiens CDNA clone KAK02706, mRNA sequence.
ACCESSION	BP270589
VERSION	BP270589.1
KEYWORDS	GI:52219938
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 581)
AUTHORS	Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,Y., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)
PUBMED	15342556
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo

4-6-1, Shitukanedai, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..581

FEATURES

Source

ORIGIN

Alignment Scores:	
Pred. No.:	3.95e-29
Score:	310.00
Percent Similarity:	98.5%
Best Local Similarity:	98.5%
Query Match:	69.2%
DB:	3
Length:	581
Matches:	64
Conservative:	0
Mismatches:	0
Indels:	1
Gaps:	0

US-10-757-745-2_COPY_54.140 (1-87) X BP270589 (1-581)

QY	1	MeGluARAlAlenuAseTyrzheGluProProValGluGluSerAlaLeuGluArg	20
Db	388	ATGGAAGAGGCTCTGAATCTTCACTTCAGAGCTCCGGTGGAGGAGAGCGCTTGAAACGC	447
QY	21	ArgProGluThrIleSerGluProLysThrTyrValaAspleuthraEngiugluThrThr	40
Db	448	CGACCTGAAACCATCTCTGAGGCCAAGACTATGTGTGACCTAAACCAATGAAAGAAACAAC	507
QY	41	AspSerThrThrSerLysIleSerProSerGluAspThrGingingluAsn-GlySerMe	60
Db	508	GATTCACCACTCTTAATAATCAGCCCACTGAAAGATCTCAGCAAGAAAAATGGCAGCAT	567
QY	60	tpheserleuile	64
Db	568	GTTCCTCTTCATT	580

[illegible]

FEATURES	Location/Qualifiers
source	1..952
	/organism="Homo sapiens"
	/mol_type="mRNA"

Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: segreff@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?se=CS0BA10562D12_CS053712_1ec=3474.r

ORIGIN

Alignment Scores:

Pred. No.:	7.55e-29	Length:	952
Score:	310.00	Matches:	68
Percent Similarity:	90.8%	Conservative:	1
Best Local Similarity:	89.5%	Mismatches:	6
Query Match:	69.2%	Indels:	2
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BK433489 (1-952)

13 ValgunguSerAlaLeuGluArgProGluThrIleSerGluProGluThrTyVal 32
 948 GTGGAGGAGGCGCTTGGACGCCGAACTGAACTCTCTGAGCCCAAGACTATGT- 890

33 AspleuthrAnguGluThrThr-AspSerThrSerIleSerProSerGluAs 52
 889 GACCTAACCAATGAGAAACAACTGATTCACACTTCTAAATCAGCCCACTGAGAA 830

52 PThrGlnGlnGluAngIySerMetPheSerIleuIleThrTTPAsnIleAspGlyLeuAs 72
 829 TACTCAGCAGAAATGCGCAGCATGTTCTCTCTCATTAACCGAATATGATGATGATTA 770

72 PLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyIleu 87
 769 TCTAAACATCTGTCTGAGAGGCGCTGAGGCGTGTGTCTTCTACTTA 724

RESULT 135
 CN803230 965 bp mRNA linear EST 26-MAY-2004
 LOCUS ILUMIGEN MCQ 32551 Katze MMR Macaca mulatta cDNA clone
 DEFINITION IBUW:12605 5' similar to Bases 1 to 965 highly similar to human
 TTRAP (Hs.210628), mRNA sequence.
 CN803230
 ACCESSION CN803230.1 GI:47699206
 VERSION EST.
 KEYWORDS Macaca mulatta (rhesus monkey)
 SOURCE Macaca mulatta
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.
 1 (bases 1 to 965)
 MAGNESSE,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
 Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
 Iadonato,S.P.
 Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 15998449
 CONTACT: C. Magnes
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagnes@illumigen.com
 Sequenced on 2004.04.02. 780 Q20 bases.
 PCR Primers
 FORWARD: CCTCCTAAAGGAGACAAA
 BACKWARD: CACTATAGGCGCAATTGGTA
 Insert length: 965 Std Error: 0.00
 Plate: C1000288 row: D column: 11
 Seq primer: CCTCCTAAAGGAGACAAA

FEATURES

source POLYA=NO.

Location/Qualifiers

1..965
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBUW:12605"
 /sex="female"
 /dev_stage="adult"
 /lab_host="E. coli SOLR"
 /clone_lib="Katze_MMR"
 /note="Organ: brain; Vector: Uni-ZAP XR, Site 1: Ecor I,
 Site 2: Xho I; Created from StrataGene ZAP-CDNA Synthesis
 Kit (catalog #200400) and ZAP-CDNA GigaPack III Gold
 Cloning Kit (catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.:	3.35e-28	Length:	965
Score:	305.00	Matches:	59
Percent Similarity:	95.2%	Conservative:	0
Best Local Similarity:	95.2%	Mismatches:	3
Query Match:	68.1%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CN803230 (1-965)

26 SerGluProGluThrTyValAspLeuThrAsnGluGluThrThrAspSerThrThrSer 45
 2 TCTGAGCCCAAGACCTATGTTGACCTTAACCAAGAAAGAAACAACTGATTCACACCTTCT 61

46 LysIleSerProSerGluAspThrGlnGlnGluAngIySerMetPheSerIleuIleThr 65
 62 AAATCAGCCCACTCGAAGATCTCAGCAGAAAGAAAGACGATGTTCTGCTCATTAAC 121

66 TrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85
 122 TGGAAATTTGATGATGATGATCTTAACATCTGTCTGAGAGGCGTGTGTCTTC 181

96 TyIleu 87
 182 TACTTA 187

RESULT 136
 CR767008 365 bp mRNA linear EST 23-SEP-2004
 LOCUS DKZP46962436 r1.469 (synonym: pklid) Pongo pygmaeus cDNA clone
 DEFINITION DKZP46962436.5', mRNA sequence.
 CR767008
 ACCESSION CR767008.1 GI:52608718
 VERSION EST.
 KEYWORDS Pongo pygmaeus (orangutan)
 SOURCE Pongo pygmaeus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Hominidae; Pongo.
 1 (bases 1 to 365)
 ANSORGE,W., Krieger,S., Regier,T., Rittmuller,C., Schwager,B.,
 Mewes,H.W., Well,B., Amlid,C., Oesanger,A., Fobo,G., Han,M. and
 Wiemann,S.
 Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regier,T., et al.)
 Unpublished (2004)
 CONTACT: MIPS

TITLE JOURNAL

AUTHORS

REFERENCE

COMMENT

MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ),
 Email: s.wiemann@dkfz-heidelberg.de, rlin, Germany. Please contact
 DKFZ for ordering:
 http://www.rzpd.de/cgi-bin/products/ci.cgi?cloneid=DKZP46962436
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES
source

Location/Qualifiers
1.365
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZP469G2436"
/tissue_type="Kidney"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: SfilA; Site_2: SfilB"

ORIGIN

Alignment Scores:

Pred. No.: 7,376-28 Length: 365
Score: 298.00 Matches: 60
Percent Similarity: 95.2% Conservative: 0
Best Local Similarity: 95.2% Mismatches: 3
Query Match: 66.5% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR767008 (1-365)

QY 1 MetGUARGAlaleuanserTYrPheGluPProPovaIGluGserAlaleuGluArg 20
DB 176 ATGGAAGGGCTCTGAACCTCTACTCGAGCTCCGGTGAAGANAGCCCTTGAAACG 235
QY 21 ArgPProGluThrIleSerGluProlyThrTYrValAspLeuThrAsnGluThrThr 40
DB 236 CCGCCCTGAAACCATCTCTGAGCCCAAGACCTATGTTCCTTAACCAATGAGAAACACT 295
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGluGluGluGluSerMet 60
DB 236 GATTCACACACTCTTAATAATGAGCCCATCTGAAGATACAGCAAGAAATGCGACATG 355
QY 61 PheSerLeu 63
DB 356 TCCTCTCTC 364

RESULT 137

R14990 416 bp mRNA linear EST 13-APR-1995
LOCUS YG45C1.r1 Soares infant brain IN1B Homo sapiens cDNA clone
DEFINITION IMAGE:35717 5', mRNA sequence.

ACCESSION R14990
VERSION R14990.1 GI:769263
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 416)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

High quality sequence stops: 277 Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1716 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 277.

FEATURES
source

Location/Qualifiers
1.416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="DB:408218"
/db_xref="taxon:9606"
/clone="IMAGE:35717"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain IN1B"
/note="Organ: whole brain; Vector: Lactamid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5'
AAGTGAAGAATTCGCGCGCCGAGGAATTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lactamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 2,126-27 Length: 416
Score: 295.00 Matches: 78
Percent Similarity: 86.8% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 5
Query Match: 65.8% Indels: 8
DB: 8 Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x R14990 (1-416)

QY 1 MetGUARGAlaleuanserTYrPheGluPProPovaIGluGserAlaleuGluArg 20
DB 96 ATGGAAGGGCTCTGAACCTCTACTCGAGCTCCGGTGAAGANAGCCCTTGAAACG 154
QY 21 ArgPProGluThrIleSerGluProlyThrTYrValAspLeuThrAsnGluThrThr 40
DB 155 GAGCTGAAACCATCTCTGAGCCCAAGACCTATGTTCCTTAACCAATGAGAAACACT 214
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGluGluGluGluSerMet 60
DB 215 GATTCACACACTCTTAATAATGAGCCCATCTGAAGATACAGCAAGAAATGCGACATG 274
QY 60 PheSerLeu-IleThrTrp-AsnIle-AspGlyLeuAsp--LeuAsnAsnLeu-SerG 78
DB 275 GTTCTCTCTCATTAATCTGGAATATTTGATGATTAAGATCTTAACAATCTGTGCG 334
QY 78 IuArg--AlaArgGlyValCys 84
DB 335 AGGAGGGGAGTCTGAGGGGGGTGTGT 357

RESULT 138

BF243927 751 bp mRNA linear EST 14-NOV-2000
LOCUS BF243927
DEFINITION 601877278P1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105866 5',
mRNA sequence.

ACCESSION BF243927
VERSION BF243927.1 GI:1157869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 751)

TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bde-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LINC988 row: k column: 19
 High quality sequence stop: 533.
 Location/Qualifiers

FEATURES

source
 1..751
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4105866"
 /tissue="type:from acute myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_id="NIH_MGC_55"
 /note="Organ: Bone marrow; Vector: pDNR-LIB (Clontech);
 site_1: SfiI (ggcgctcgcc); Site 2: SfiI
 (ggccatcgcc); Double stranded cDNA was prepared from
 cell line K562. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGGC-3' and
 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.65 kb (range 0.5-4.0 kb). 14/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

ORIGIN

Alignment Scores:

Pred. No.: 2,326-26 Length: 751
 Score: 28950 Matches: 80
 Percent Similarity: 89.3% Conservative: 0
 Best Local Similarity: 89.3% Mismatches: 7
 Query Match: 94.6% Indels: 7
 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BF243927 (1-751)

QY 1 MetGlaArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 152 ATGGAAAGGCTCTGAACCTCTACTCTGAGCTCCGTTGAGAGAGAGCCCTTGAGAGCC 211
 QY 21 ArgProGluThrIleSerGluProValThr-TyrValAspLeuThrAsnGluGluThrTh 40
 DB 212 CGACT-GAAACCATCTCTAGCCCAAGACCTTATCTTGACCTTAACCAATGAGAAAAACT 270
 QY 40 TAspSerThrSerIleSerProSerGluAspThrGluGluAsnGlySerMe 60
 DB 271 GGAATCCACCAT-TCMAATTCAG-CGATCTGAGATCT-CAGCAAGAAAAATGGACGCT 327
 QY 60 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluVal 80
 DB 328 GTC-TCTCTCAATACCTGAAATTTGATGATTAATCAATCTGTCTGAGAGGGCC 386
 QY 80 ATGCTVal-CysSerTyrLeu 87
 DB 387 TCGAGGGGTGCTCTCTACTTA 409

RESULT 139

BM623866 898 bp mRNA linear EST 18-APR-2001
 LOCUS 60249018F1 NIH_MGC_79 Homo sapiens CDNA clone IMAGE:4770389 5',
 DEFINITION BM623866 sequence.
 ACCESSION BM623866
 VERSION BM623866.1 GI:13675237
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 898)
 AUTHORS NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csaplos-remail@llnl.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LINC1637 row: d column: 06
 High quality sequence stop: 688.
 Location/Qualifiers

FEATURES

source

1..898
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4770389"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_id="NIH_MGC_79"
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
 site_1: SfiI (ggcgctcgcc); Site 2: SfiI
 (ggccatcgcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGC-3'
 and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.3
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4,566-26 Length: 898
 Score: 288.00 Matches: 56
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 64.3% Indels: 0
 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BM623866 (1-898)

QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerIleSerProSerGlu 51
 DB 440 GTTGACCTTAACCAATGAGAAACAACCTGATTCACCACTTAAATCAGCCCATCTGAA 499
 QY 52 AspThrGluGluGluAsnGlySerMetPheSerLeuIleThrTyrAsnIleAspGlyLeu 71
 DB 500 GATCTCTAGAGAGAAAAATGGACGATGTTCTCTCTCAATACCGAATATGATGATTA 559
 QY 72 AspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
 DB 560 GATCTAAACAATCTGTCAAGAGGCTCGAGGGGTGTGTCCTACTTA 607

RESULT 140

BM539358 635 bp mRNA linear EST 20-FEB-2002
 LOCUS hb08d09.g1 Canis CDNA from testes cells Canis familiaris cDNA
 DEFINITION hb08d09 5', mRNA sequence.
 ACCESSION BM539358
 VERSION BM539358.1 GI:18821216
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.
 1 (bases 1 to 635)
 O'Shaughnessy,A.L., McCombie,W.R., Baker,D.P., Balija,V.,

REFERENCE	1 (bases 1 to 645)
AUTHORS	Cogburn, L.A., Morgan, R. and Burnside, J.
TITLE	ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal Genome Project
JOURNAL	Unpublished (2002)
COMMENT	Contact: Larry A. Cogburn

University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburnudel.edu, www.chickens.udel.edu.

FEATURES

Source
Location/Qualifiers
1. 645
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler, Ottawa Research Centre, leghorn"
/db_xref="taxon:9031"
/clone="pGf2n.pk002.c6"
/sex="Male and Female"
/tissue_type="Abdominal Fat"
/dev_stage="Embryonic (d18,d19); post-hatch (d1,w3,w7,w9,w16,y1)"
/lab_host="E. coli EMDH10B"
/clone_lib="Normalized Chicken Abdominal Fat Library (pGf2n)"
/note="Vector: PCMVSPORT6; Library made from equivalent pools of total RNA isolated from each developmental age (across strains); Single pass sequencing from 5'-end"

ORIGIN

Alignment Scores:

Pred. No.: 4,546-18 Length: 645
Score: 224.00 Matches: 46
Percent Similarity: 70.1% Conservative: 15
Best Local Similarity: 52.9% Mismatches: 24
Query Match: 50.0% Indels: 2
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BM426270 (1-645)

QY 1 MetGUAArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 196 CTGGAGAGGGCGGCTGAGCCCTTCAAGCGCGCGATGACAGCGCGCGCGCG 255
QY 21 ArgProGluThrIleSerGluProLySerTyValAspLeuThrAsnGluThr 40
Db 256 GCAGAGAGGGGCTCGCGGGCGCTGGAAGCTGTATTACCTCACACAGATGATCTCA 315
QY 41 AsperThrSerIleSerProSerGluAspThrGluGluGluSerMet 60
Db 316 AGTAATACCGACAGC-----AGTGTGCGACGCTCCAGCAACAAGATGATGACAGCAGC 369
QY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 370 TTCTCGCTGATTAATTGGAACTTGTGGCTGGAGCTGGGGAATCTGCAGAGGAGCT 429
QY 81 ArgGlyValCysSerTyIleu 87
Db 430 AAGGTGTCTGTTCTTACCTG 450

RESULT 143

CN642527 1087 bp mRNA linear EST 12-MAY-2004
LOCUS CN642527
DEFINITION ILUMIGEN MC0 6530 Katze MPPL2 Macaca mulatta cDNA clone IBUM:4699
(Hs.210628), mRNA sequence.
ACCESSION CN642527.1 GI:47153537
VERSION
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Macaca mulatta
Bukayvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.

REFERENCE

AUTHORS
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.

TITLE
JOURNAL
PUBLISHED
COMMENT
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
15996449
Contact: C. Magness
11umigen Biosciences Inc. 450, Seattle, WA 98134, USA
2205 Alameda Way S, Suite 400
Tel: 2063780408
Fax: 2063780408
Email: csmagness@11umigen.com
Sequenced on 2003.12.24. 840 Q20 bases.
Perkinmerer CCTGCTAAGAGGAGACAAA
FORMARD CCTGCTAAGAGGAGACAAA
BACKWARD CACTATGCGCGAATTGCGTA
Insert Length 1087 Std Error: 0.00
Plate: CL000006 Row: D Column: 10
Seq primer: CCTGCTAAGAGGAGACAAA
POLYA=No.

FEATURES

Source
Location/Qualifiers
1. 1087
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian 9544"
/db_xref="taxon:9544"
/clone="IBUM:4699"
/sex="male"
/dev_stage="newborn infant"
/lab_host="E. coli SOLR"
/clone_lib="Katze MPPL2"
/note="Organ: Placenta; Vector: Uni-ZAP XR; Site 1: EcoR
I; Site 2: Xho I; Created from Strategene ZAP-CDNA
Synthesis Kit (catalog #200400) and ZAP-CDNA Gigapack III
Gold Cloning Kit (Catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.: 2,186-17 Length: 1087
Score: 221.00 Matches: 43
Percent Similarity: 93.5% Conservative: 0
Best Local Similarity: 93.5% Mismatches: 3
Query Match: 49.3% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CN642527 (1-1087)

QY 42 SerThrThSerIleSerProSerGluAspThrGluGluGluSerMetPhe 61
Db 2 TCCACGCACTTCAAAATCAGCCCATCTGAAGATACCTCAGCAAAAATGACGATGTTTC 61
QY 62 SerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 81
Db 62 TGCTTCATTAACCTGGAATATGATGATTGATCTAAACATCTGTCAAGAGGAGCTGA 121
QY 82 GlyValCysSerTyIleu 87
Db 122 GGGGTGTGTTCTTACTTA 139

RESULT 144

Bu471395 625 bp mRNA linear EST 30-NOV-2002
LOCUS Bu471395
DEFINITION 603363114F1 CSEORBN21 Gallus gallus cDNA clone CHEST258k3 5', mRNA
sequence.
ACCESSION Bu471395.1 GI:25964972
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

AUTHORS
Boardman, P.E., Sanz-Bzquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, M.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
COMMENT Contact: Simon Hubbard
Department of Biomedical Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES
source 1..625
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST258K3"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBN21"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:
Pred. No.: 1,41e-17 Length: 625
Score: 220.00 Matches: 45
Percent Similarity: 69.0% Conservative: 15
Best Local Similarity: 51.7% Mismatches: 25
Query Match: 49.1% Indels: 2
DB: 5 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BU471395 (1-625)

QY 1 MetGUAAGAAlaLeuanserTyrPheglupropovalGluGluseralaleuGluary 20
Db 109 CTGAGAGAGGCGCTGAGCGCTTCTTGAAGCGCGCATAAACAGACAGACGCGCGCGCG 168
QY 21 ArgProglutThrIleSerGluProlysthrTyrValaspLeuThrAsnGluGluThr 40
Db 169 GCAGAGAGGCGCGCTGAGCGCGCTGAGCGCTGATGATGATGATGATGATGATGATGATG 228
QY 41 AspSerThrThrSerIleSerProserGluAspThrGlnGlnGluAsnGlySerMet 60
Db 229 AGTAATACCAAGAGC-----AGTGTGCAAGCTCAACCAACCAAGATGATGACAGCAGC 282
QY 61 PheSerleuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgala 80
Db 283 TTCTGCGTATACCTTGAACATTGATGAGGCTGAGACTGGGGAATCTGACAGAGCGAGCT 342
QY 81 ArgGlyValCysSerTyrLeu 87
Db 343 AGAGGTGTCTGTTCTTACCTG 363

RESULT 145
LOCUS BI067773 662 bp mRNA linear EST 15-JUN-2001
DEFINITION pgfin.pk007.d9 normalized chicken fat cDNA library Gallus gallus
CDNA clone pgfin.pk007.d9 5' similar to gi11418470

ref|XP_004263.1| TRAF and TNF receptor-associated protein. [Homo sapiens] emb|CA11141.1| (A1031775) dJ30M3.3 (novel protein similar to C. elegans Y65D3A.4) [Homo sapiens] emb|CA92966.1| (A2269473) TRAF and TNF receptor associated prote, mRNA sequence.

ACCESSION BI067773 GI:14475295
VERSION EST
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauia; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 662)

REFERENCE
AUTHORS Cogburn, L.A., Morgan, R.W. and Burnside, J.
TITLE Chicken ESTs from fat
JOURNAL Unpublished (2001)
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
source 1..662
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgfin.pk007.d9"
/sex="Male and Female"
/tissue_type="fat"
/lab_host="E.coli EMDH10B"
/clone_lib="normalized chicken fat cDNA library"
/note="Vector: pSPORT1"

ORIGIN

Alignment Scores:
Pred. No.: 1,53e-17 Length: 662
Score: 220.00 Matches: 45
Percent Similarity: 69.0% Conservative: 15
Best Local Similarity: 51.7% Mismatches: 25
Query Match: 49.1% Indels: 2
DB: 2 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BI067773 (1-662)

QY 1 MetGUAAGAAlaLeuanserTyrPheglupropovalGluGluseralaleuGluary 20
Db 118 CTGAGAGAGGCGCTGAGCGCTTCTTGAAGCGCGCATAAACAGACAGACGCGCGCGCG 177
QY 21 ArgProglutThrIleSerGluProlysthrTyrValaspLeuThrAsnGluGluThr 40
Db 178 GCAGAGAGGCGCGCTGAGCGCGCTGAGCGCTGATGATGATGATGATGATGATGATGATG 237
QY 41 AspSerThrThrSerIleSerProserGluAspThrGlnGlnGluAsnGlySerMet 60
Db 228 AGTAATACCAAGAGC-----AGTGTGCAAGCTCAACCAACCAAGATGATGACAGCAGC 291
QY 61 PheSerleuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgala 80
Db 222 TTCTGCGTATACCTTGAACATTGATGAGGCTGAGACTGGGGAATCTGACAGAGCGAGCT 351
QY 81 ArgGlyValCysSerTyrLeu 87
Db 352 AGAGGTGTCTGTTCTTACCTG 372

RESULT 146
LOCUS BU468774 946 bp mRNA linear EST 30-NOV-2002
DEFINITION 603571865F1 CSEQRBN20 Gallus gallus cDNA clone CHEST279b17 5', mRNA
sequence.
ACCESSION BU468774
VERSION BU468774.1 GI:25962351
KEYWORDS EST.

SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 946)
REFERENCE Boardman, P.E., Sant-Ezquerro, J., Overton, I.M., Burr, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
JOURNAL PUBMED
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST) 88, Manchester, M60 1QD, UK
Tel: 0161 275 0830
Fax: 0161 275 0409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
FEATURES
source
1..946
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST2/9b17"
/sex="Male and Female"
/tissue_type="Chondrocytes isolated from growth plate
cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1fb="CSEORBN20"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI;
Site_2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylation C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunt-ended, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldi et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."

ORIGIN
Alignment Scores:
Pred. No.: 2,82e-17 Length: 946
Score: 219.50 Matches: 46
Percent Similarity: 71.3% Conservative: 16
Best Local Similarity: 52.9% Mismatches: 22
Query Match: 49.0% Indels: 3
DB: 5 Gaps: 2
US-10-757-745-2_COPY_54_140 (1-87) x BU648774 (1-946)
QY 1 MetGUAAGAAlaLeuAenSerTYrPhGluPProVaIGluSeRaLaLeuGluAry 20
Db 60 CTGAGAGAGGCGCTGAGCGCTACTTTGAGCGCGGATGAACGAGCGCGCGCGCA 119
QY 21 ArgPrgGluThrIleSerGluPProLyThrTYrValAspLeuThraAngluGluThr 40
Db 120 GAGAGGAGACTCG--GCGGGGCTGAGAGCTGTATTGACCTCAAGAGATGATATCGCA 176
QY 41 AspSerThrThSerIySileSerProSerGluuAepThrGInGInGluuAnglySerMet 60
Db 177 AGTATATACACAGC-----AGTGGTGCAGACCTCAAGCACAAGATGATGACACAC 230
QY 61 PheSerLeuIleThrTIPaenIleAspGlyLeuAspLeuAenAenLeuSerGluArya 80
Db 231 TTCTCGCTGATTAACCTTGAGACATTGATGGCTGAGACTGGGGAATCTGCAGAGCGAGCT 290

QY 81 ArgGlyValCySeSerTYrLeu 87
Db 291 AGAGGTCTCTCTTCTTACTCTG 311
RESULT 147
BI064472
LOCUS
DEFINITION
BI064472 600 bp. mRNA. 1 near EST 15-JUN-2001
pGfin.pk001.h17 normalized chicken fat cDNA library
cDNA clone pGfin.pk001.h17 5' similar to g11705262
ref|NP_057698.1| TRAP and TMR receptor-associated protein [Homo
sapiens]g, mRNA sequence.
ACCESSION
BI064472 GI:14471994
VERSION
BI064472.1
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 600)
REFERENCE Cogburn, L.A., Morgan, R.W. and Burnside, J.
Chicken ESTs from fat
Unpublished (2001)
JOURNAL
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburnudel.edu, www.chickest.udel.edu.
Location/Qualifiers
FEATURES
source
1..600
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pGfin.pk001.h17"
/sex="Male and Female"
/tissue_type="fat"
/lab_host="E.coli EMDH10B"
/clone_1fb="normalized chicken fat cDNA library"
/note="Vector: pSPORT1"

ORIGIN
Alignment Scores:
Pred. No.: 2.8e-17 Length: 600
Score: 217.50 Matches: 46
Percent Similarity: 71.3% Conservative: 16
Best Local Similarity: 52.9% Mismatches: 22
Query Match: 48.5% Indels: 3
DB: 2 Gaps: 2
US-10-757-745-2_COPY_54_140 (1-87) x BI064472 (1-600)
QY 1 MetGUAAGAAlaLeuAenSerTYrPhGluPProVaIGluSeRaLaLeuGluAry 20
Db 65 CTGAGAGAGGCGCTGAGCGCTACTTTGAGCGCGGATGAACGAGCGCGCGCGCA 124
QY 21 ArgPrgGluThrIleSerGluPProLyThrTYrValAspLeuThraAngluGluThr 40
Db 125 GAGAGGAGACTCG--GCGGGGCTGAGAGCTGTATTGACCTCAAGAGATGATATCGCA 181
QY 41 AspSerThrThSerIySileSerProSerGluuAepThrGInGInGluuAnglySerMet 60
Db 182 AGTATATACACAGC-----AGTGGTGCAGACCTCAAGCACAAGATGATGACACAC 235
QY 61 PheSerLeuIleThrTIPaenIleAspGlyLeuAspLeuAenAenLeuSerGluArya 80
Db 236 TTCTCGCTGATTAACCTTGAGACATTGATGGCTGAGACTGGGGAATCTGCAGAGCGAGCT 295
QY 81 ArgGlyValCySeSerTYrLeu 87
Db 296 AGAGGTCTCTCTTCTTACTCTG 316

RESULT 148
BZ858137
LOCUS BZ858137 577 bp DNA linear GSS 18-MAR-2003
DEFINITION CH240_232018.TV CHORI-240 Bos taurus genomic clone CH240_232018,
genomic survey sequence.
ACCESSION BZ858137
VERSION BZ858137.1 GI:29085542
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 577)
Zhao, S., Shetty, U., Shatsman, S., Tsagaye, G., Geer, K.,
Shvartsbeyn, A., Gebregiorgis, E., Chen, D., Riggs, F., de Jong, P.,
Crawford, A.M. and McEwan, J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished (2003)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pjejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by AgResearch Ltd., New Zealand and the
Institute of Genomic Research (TIGR), USA.
Plate: 232 row: 0 column: 18
Seq primer: T7
Class: BAC ends.

FEATURES

source

1..577
Location/Qualifiers
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_232018"
/sex="Male"
/cell_type="Blood"
/clone_1ib="CHORI-240"
/note="Vector: PTARBAC1.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Alignment Scores:

Pred. No.: 3,08e-17 Length: 577
Score: 217.00 Matches: 44
Percent Similarity: 82.8% Conservative: 4
Best Local Similarity: 75.9% Mismatches: 8
Query Match: 48.4% Indels: 2
DB: 9 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BZ858137 (1-577)

OY 32 VALAAPLEUThraAngluThrThraPseThrThraSerlyleSerProSerGu 51
DB 83 GTTGACCTAACAGAGAAACAAATATTCATTAGTTTAAACCGACATCTGA 142
OY 52 ACP-----ThgInglIngluAnnglySerMetPheSerLeuileThrTripanileAp 69
DB 143 GATTAAGCTTCAGCAAGACATGCACTGATTTCTTTCAATTCCTGGAATATTGAT 202
OY 70 GtyleuApLeuAnAnleuSerGuArgAlaArglyValCyseSerTyrlen 87
|||||.....|

DB 203 GGATTGCATGACATCAATCTCTTAGAGAGGGCTCCAGGGGTGTCTTATTTA 256

RESULT 149
AM669835
LOCUS AM669835 549 bp mRNA linear EST 25-APR-2001
DEFINITION 113421.MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AM669835
VERSION AM669835.1 GI:7526349
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 549)
Smith, T.P.L., Grosse, W.M., Fréking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Petrea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCATGACCAT
BACKWARD: GTTTCACGACGACGACG
Plate: 108 row: M column: 18
Seq primer: ATTGAGTGCATCTATG.
Location/Qualifiers
1..549
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1ib="MARC 1BOV"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

FEATURES

source

1..549
Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1ib="MARC 1BOV"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

ORIGIN

Alignment Scores:

Pred. No.: 9.38e-17 Length: 549
Score: 213.00 Matches: 43
Percent Similarity: 82.5% Conservative: 4
Best Local Similarity: 75.4% Mismatches: 8
Query Match: 47.5% Indels: 2
DB: 1 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x AM669835 (1-549)

OY 32 VALAAPLEUThraAngluThrThraPseThrThraSerlyleSerProSerGu 51
DB 312 GTTGACCTAACAGAGAAACAAATATTCATTAGTTTAAACCGACATCTGA 371
OY 52 ACP-----ThgInglIngluAnnglySerMetPheSerLeuileThrTripanileAp 69
DB 372 GATTAAGCTTCAGCAAGACATGCACTGATTTCTTTCAATTCCTGGAATATTGAT 431
OY 70 GtyleuApLeuAnAnleuSerGuArgAlaArglyValCyseSerTyrlen 86
DB 432 GGATTGCATGACATCAATCTCTTAGAGAGGGCTCCAGGGGTGTCTTATTAT 482
|||||.....|

Thu Mar 16 10:39:27 2006

us-10-757-745-2__copy_54_140.rvt

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RESULT 150
CN233559
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CN233559
RjallFP02.ab1 RJbrain Gallus gallus CDNA 5', mRNA
CN233559
CN233559.1 GI:46337203 -
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 531)
Savolainen, P., Flitzsimmons, C.J., Arvestad, L., Andersson, L. and
Lundeberg, J.
EST analyses of brain and testis cDNA libraries from white leghorn
and Red Jungle Fowl
Unpublished (2004)
Contact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0) 8 5537 8481
Fax: +46 (0) 8 5537 8315
Email: Peter.savolainen@biotech.kth.se
Seq primer: M13 reverse primer.

```

FEATURES
  source
    Location/Qualifiers
      1..531
        /organism="Gallus gallus"
        /mol_type="mRNA"
        /strain="Red JUNGLEFOW1"
        /db_xref="taxon:9031"
        /sex="female"
        /label="ElectroMAX DH10B (Invitrogen)"
        /rdb_name="RedJ1"
        /note="Organ Brain Vector: pSPOR-1; Site 1: Hind III
        site 2: EcoRI. The cDNA libraries were created with the
        Superscript Plasmid System (Invitrogen)."
ORIGIN

Alignment Scores:
Pred. No.:
Score: No.:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

```

US-10-757-745-2_COPY_54_140 (1-87) X CN233559 (1-531)

OY	1	MetGluAlaLeuAlaLeuAsnSerIyrPheGluProVal---	GlucIserAlaLeuGlu	19
Db	123	CTGGAGAGGGGGCTGGAGCCCTACTTTAGGCCCCAT	TAACAGACAGACAGAGCGGGG	182
OY	20	ArgAGProGluThrIleSerGluProIysThrValAsp	LeuThrAsnGluIuThr	39
Db	183	GGCGCAGAGGGGGCTCGCGGGGCTGAAAGCTG	ATTGATGACTCAGCAGCATGTATCT	242
OY	40	ThrAspSerThrSerIyrIleSerProSerCila	AspThrGluGluAsnGlySer	59
Db	243	GGAACTATTACGACGACG-----AGTGGTSC	AGACTCCAGACCTCCACCAACAAACAAAGATG	296
OY	60	MetPheSerLeuIleThrTTPAsnIleAspGly	LeuAspLeuAsnAsnLeuSerGluArg	79
Db	297	ACCTTCCTCGCTGAAATTAATTGGAACTGAT	TGGCTGGACCTGGGGAATCTGCGAGGCGA	356
OY	80	AlaArgGlyValCysSerIyrLeu	87	
Db	357	GCTAGAGGTGCTCTGTTCTTACCTG	380	
RESULT 151				
BU406549				
LOCUS	..	BU406549	782 bp	mrna linear EST 27-NOV-2002

DEFINITION 603483616f1 CSECHCN59 Gallus gallus cDNA clone CNE57374p3.5', mRNA sequence.

ACCESSION BU406549

VERSION BU406549.1 GI:25775605

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Enxaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Phasiantia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 782)

Boardman, P.H., Sanz-Ezquerro, J., Ovelton, I.M., Burt, D.W., Bosch, E., Fong, M.T., Tickle, C., Brown, R.A., Hallin, S.A. and Hubbard, S.J. A Comprehensive Collection 1969 (2002)

Curr. Biol. 12 (22)

12445392

COMMENT Contact: Simon Hubbard

Department of Biomedical Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1OD, UK

Tel: 01612008930

Fax: 01612350490

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

FEATURES

source 1..782 src=gallus-gallus

```

/organism="Gallus gallus"
/mol_type="cRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="chsr374d3"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSECOCHN59"
/notes="Organ: limbs; This vector: pBluescript II KS(+); Site:1: EcoRI; Site:2: NotI; This normalized library was constructed from 1 million independent clones; cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used."

```

ORIGIN

Alignment Scores:		Length:	782
Pred. No.:	1,73e-16	Matches:	45
Score:	212.50	Conservative:	17
Percent Similarity:	70.5%	Mismatches:	23
Best Local Similarity:	51.1%	Indels:	3
Query Match:	47.4%	Gaps:	2
Da:	5		

```

US-10-757-745-2_COPY_54_140 (1.87) x BU0406549 (1.782)
OY      1 MetGluuYrgAlaLeuAmSerTyrPheGlaIPProProVal---GluGluSerAlaLeuGlu 19
Db      165 CTGGAGAGGGCGCGCTGAGACCCCTACTTGTAGAGCCCCCATATAMGAGACAGACGAGCGCGG 224
OY      20 ATGAGTProGluThrIleSerGluuProLysThrTyrValAspLeuThrAsnGluuThr 39
Db      225 GCGGAGGAGGGGGCGTCCGCGGGGCGTGGAACTGATTGACCTCAGCAGCATGTACT 284
OY      40 ThrAspSerThrIleSerYsIleSerProSerGlaAspThiGlnGlnGluAsnGlySer 59
Db      285 GCAAGTAAATCCAGCAGC-----AGTGTGTCAGACCTCCAAACCAAGATGATGACAC 338
OY      60 MetPheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArg 79

```


2-SEP-2001

Page 88

FEATURES	Location/Qualifiers
source	1. .691

ORIGIN

Pred. No.:	1.97e-16	69
Score:	211.50	Length:
Percent Similarity:	66.3%	Matches:
Best Local Similarity:	52.5%	Conservative:
Query Match:	47.2%	Mismatches:
DB:	3	Indels:
		Gaps:
		1

US-10-757-745-2_COPY_54_140 (1-87) X B1648868 (1-691)

```

OY 2 GUAGAGAlaleuAanSerTYrPheGluProProValGluGluSerAlaleuGluArg 21
Db 9 CAGAAAGCCCTGAGGGCTACTTCGAGCTGCAGAGAACACCAAGGGTGGCCGGCCAG 68
OY 22 ProGUuThrTleSerGluProLYrThrTYrValAspLeuThrArgGluGluThrAsp 41
Db 69 CCTCCACGCTCCTTCAGATCCAGGCCCTATGTATCTACACCAAGAGATGCATAATAT 122
OY 42 SerThrThrSerLYrTleSerProSerGluAspThrGlnGlnGluAanLYrSerMetPhe 61
Db 129 ACACACATTTTAAAGGCCAGCTCATCT--GGAACTCCTCTAGAAAGTACAGCACTATT 188
OY 62 SerLeuTleThrTPaenTleAspGlyLeuAspLeuAanAanLeuSerGluArgAlaArg 81
Db 186 TCTTTCATTACTGGAAATATGAAATGAAATGAGATGCAAATCTGCCAGAGGGCTCGA 244
OY 82 GlyValCYrSerTYrLeu 87
Db 246 GGGAGTGTGTTCTGGCTTA 263

```

REFERENCE	1 (pages 1 to 767)
AUTHORS	Williams, C., Wirta, V., Richter, K., Karlsson, C., Lundberg, J. and Carlsson, L
TITLE	Expressed sequence tags of cDNA clones from a hematopoietic stem cell line expressing <i>hbx2</i>
JOURNAL	Unpublished. (2005)
COMMENT	Contact: Williams, C.

**Institution of Biotechnology
Alnövra University Center, KTH-Royal Institute of Technology, 100
31 Stockholm, Sweden
Tel.: +4685378332.
Fax: +4685378481.
Email: cecilia.williams@biotech.kth.se
Seq primer: M13REV.**

FEATURES	Location/Qualifiers
source	1. .767

```

/sex="Male and Female"
/clisue_type="Bone Marrow"
/cell_type="Hematopoietic progenitor/stem cells
immortalized by Lhx2"
/bcell_line="hematopoietic stem cell-like cell line
Bcell-3"
/donorsage="adult"
/clone_idb="Mus Musculus hematopoietic BM-HPCS CDNA
library"
/note="Organ: Bone Marrow; Vector: pCMVSPORT.1;
Preamplified custom cDNA library by Invitrogen/Resen

```

ORIGIN

Pred. No.:	2,26e-16
Length:	76
Matches:	21,150
Conservative:	66,3%
Mismatch:	52,3%
Indels:	47,2%
Query Match:	8
GB:	1

US-10-757-745-2_COPY_54_140 (1-87) X CX226137 (1-767)

[illegible]

QY 82 G1yValCyseTyrLeu 87
|||||
Db 425 GGAGTGTCTCCTGCTA 442

RESULT 159
BF784792 841 bp mRNA linear EST 12-JAN-2001
LOCUS 60211139F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239537
DEFINITION 5', mRNA sequence.
ACCESSION BF784792
VERSION BF784792.1 GI:12089828
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 841)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9852 row: m column: 10
High quality sequence stop: 719.
Location/Qualifiers
1..841
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4239537"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library." "

FEATURES
source
1..841
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4239537"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library." "

ORIGIN

Alignment Scores:

Pred. No.: 2,55e-16 Length: 841
Score: 211.50 Matches: 45
Percent Similarity: 66.3% Conservative: 12
Best Local Similarity: 52.3% Mismatches: 28
Query Match: 47.2% Indels: 1
Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BF784792 (1-841)

QY 2 GUATGATATLeuAsnSerTyRPhgGluProProValGluGluSerAlaLeuGluArgArg 21
|||||
Db 236 CAGAAAGCCCTGAGCCCTACTTCGAGTCGCGAGAACGACGACGAGGCGCGCCGCG 295
|||||
QY 22 ProGluThrIleSerGluProLysThrTyRValAspLeuThrAsnGluGluThrThrAsp 41
|||||
Db 296 CCTCCACGCTCCTTCAAGTCGAGGCGCTATGTTGATCTAACCAACGAGATGCAATGAT 355
|||||
QY 42 SerThrThrSerIleSerProSerGluAspThrGluGluAsnGluSerMetPhe 61
|||||
Db 356 ACAACATTTAGAACCCAGTCATCT---GGAATCCTCTAGACATAGCACCATATT 412
|||||
QY 62 SerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
|||||
Db 413 TCTTCATTAACCTGGAATATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 472

QY 82 G1yValCyseTyrLeu 87
|||||
Db 473 GGAGTGTCTCCTGCTA 490

RESULT 160
BG298330 942 bp mRNA linear EST 21-FEB-2001
LOCUS 602397112F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511666 5',
DEFINITION mRNA sequence.
ACCESSION BG298330
VERSION BG298330.1 GI:13062875
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 942)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM10395 row: h column: 03
High quality sequence stop: 715.
Location/Qualifiers
1..942
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:4511666"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, oligo-dt primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library." "

FEATURES

source
1..942
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:4511666"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, oligo-dt primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library." "

ORIGIN

Alignment Scores:

Pred. No.: 2,96e-16 Length: 942
Score: 211.50 Matches: 45
Percent Similarity: 66.3% Conservative: 12
Best Local Similarity: 52.3% Mismatches: 28
Query Match: 47.2% Indels: 1
Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BG298330 (1-942)

QY 2 GUATGATATLeuAsnSerTyRPhgGluProProValGluGluSerAlaLeuGluArgArg 21
|||||
Db 232 CAGAAAGCCCTGAGCCCTACTTCGAGTCGCGAGAACGACGACGAGGCGCGCCGCG 291
|||||
QY 22 ProGluThrIleSerGluProLysThrTyRValAspLeuThrAsnGluGluThrThrAsp 41
|||||
Db 292 CCTCCACGCTCCTTCAAGTCGAGGCGCTATGTTGATCTAACCAACGAGATGCAATGAT 351
|||||
QY 42 SerThrThrSerIleSerProSerGluAspThrGluGluAsnGluSerMetPhe 61
|||||
Db 352 ACAACATTTAGAACCCAGTCATCT---GGAATCCTCTAGACATAGCACCATATT 408
|||||
QY 62 SerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
|||||
Db 409 TCTTCATTAACCTGGAATATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 468

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	ATTNRS	TITLE	JOURNAL	COMMENT
82	GIYValCysSerTyrLeu 87										
Db	469 GGGGGTGTCTCTGACCTA 486										
RESULT 161											
BI656151	603283518r1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5327572 5',	963 bp	MRNA	linear	EST 12-SRP-2001						
LOCUS	BI656151										
DEFINITION	MRNA sequence.										
ACCESSION	BI656151										
VERSION	BI656151.1										
KEYWORDS	GI:15570387										
SOURCE	EST										
ORGANISM	Mus musculus (house mouse)										
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
ATTNRS	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;										
TITLE	Sciurionathi; Murioidea; Muridae; Murinae; Mus.										
JOURNAL	1 (bases 1 to 963)										
COMMENT	NIH-MGC http://mgs.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contract: Robert Strausberg, Ph.D. Email: gcgaps-remail.nih.gov Tissue Procurement: Lochar Hemmighausen Ph.D., Priscilla Furch Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Inyte Genomics Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://imgc.lnl.gov:4 column: 05 plate: LNL01831 High quality sequence group: 693. Location/Qualifiers 1 963 "organism="Mus musculus" "mol_type="mRNA" "status="NM_001" "db_xref="taxon:10090" "clone IMAGE:5327572" "tissue_type="tumor, gross tissue" "dev_stage="5 months" "lab_host="DH10B" "clone_lib="NCI_CGAP_Mam4" "note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; Library 2: NCI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lochar Hemmighausen/Priscilla Furch, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."										

Db	422	AACAACATTTAGAAGCAGATGCATCT--GGAATCCTCTAGAAATATGACGACCTATT	483
Qy	62	Seirleuilehrrhrrpansilleapglyleuhsrpeuhsrnsrleuhserrjulyrghlaryg	81
Db	483	TCTTTCATTCACCTCGAATATTCATGATTATATGATGATGCAATCTGCCCGAAGCGGCTCGA	542
Qy	82	GlyValCysSerTyrLeu	87
Db	543	GAGGCTGTCTCTCGCTTA	560
RESULT 162			
LOCUS	CA976386	1046 bp	mRNA linear EST 06-JAN-2000
DEFINITION	AGENCOURT 8862577 NCL_CAP_Man2 Mus musculus cDNA clone		
ACCESSION	CA976386		
VERSION	CA976386.1	GI:27509040	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.		
REFERENCE	NIH-MGC http://mgi.nci.nih.gov/ .		
AUTHORS	1 (bases 1 to 1046)		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strassberg, Ph.D. Email: cgsaps-remail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov Plate: LHAM13954 row: 1 column: 06 High quality sequence scop: 348.		
FEATURES			
source	Location/Qualifiers		
	1..1046		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="FVB/N-3"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:6437549"		
	/tissue_type="tumor, biopsy sample"		
	/dev_stage="5 months"		
	/lab_host="DH10B"		
	/clone_lib="NCL_CGAP_Man2"		
	/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
ORIGIN			
Alignment Scores:	3.4e-16	Length:	1046
Pred. No.:	21,50	Matches:	45
Score:	66.3%	Cometative:	12
Percent Similarity:	52.3%	Mismatches:	28
Best Local Similarity:	47.2%	Indels:	1
Query Match:	6	Gaps:	1
Db:			
US-10-757-745-2_COPY 54_140 (1-87) x CA976386 (1-1046)			
Qy	2	GUARGAALeubanserTyrPhegluProProValgluIsuSerAlaleuGIuArgArg	21
Db	88	CGAGAGCGCTGAGCGGCTTACTGAGCGTCCAGAGACACACAGCGGTGGCGGCGCAG	147
Qy	22	ProgluThrIleSerGluProIysThrTyrValAspleuThrXenGIuGIuThrThrasp	41
Db	148	CTCCACAGCTCTTCAAGTCGAGGCTATGTGTATCTAACCAAGAGATGCAATGAT	207

```

Db          |||||
477 GGGGTGCTCTCTGCTT 494

RESULT 164
LOCUS       CB577890
DEFINITION  nrdg1-00195-c6 5', mRNA sequence.
ACCESSION   CB577890
VERSION     CB577890.1 GI:29521931
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 627)
AUTHORS    Amgen EST Program.
TITLE       Amgen Rat EST Program
JOURNAL     Unpublished (2003)
COMMENT     Contact: Dan Fitzpatrick
            Amgen, Inc
            One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00195 row: C column: 6.

FEATURES
    source
        1..627
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
            /db_xref="taxon:10116"
            /clone="nrdg1-00195-c6"
            /tissue_type="Dorsal Root Ganglia"
            /clone_id="nrdg1 (10855)"
            /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
            dorsal root ganglia"

ORIGIN
Alignment Scores:
Pred. No.:      2,33e-16      Length:      627
Score:          210.50       Matches:      45
Percent Similarity: 67.4%    Conservative: 13
Best Local Similarity: 52.3% Mismatches:    27
Query Match:    47.0%       Indels:       1
                        Gaps:       1

US-10-757-745-2_COPY_54_140 (1-87) x CB577890 (1-627)
QY      2  GUAAGAlaleuAnSeTyRPhGluProVoAlGluGluSerAlaleuGluArg 21
        :::::::::::::::::::: ||| ::|
Db      270  AAAAAAGCGTTGACGCGCTCTCTTGACACAGACAAGACGACTRAGCGCGCTCACAG 329
        :::::::::::::::::::: ||| ::|
QY      22  ProGluThrIleSerGluProLyThrTyValAspleuThraAngluThrThrasp 41
        ||| ||| ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db      330  CCTCGACATCTCTCAAGTCCGAGAGACTATGTTATCTAACCAATGAGATGCAAATGAT 389
        ||| ||| ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
QY      42  SerThrThrSerLyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
        ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db      390  ACCACCAATTTAGAAACAGTCATCTC---GGAATCTCCTTAGAAGATAGCAGACATC 446
        ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
QY      62  SerLeuIleThrTPanIleAspGlyLeuAspleuAsnIleuSerGluArgAlaArg 81
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      447  TCTTTCATTACCTGGAATATTGATGATGATGATGATGATGATGATGATCCAGAGAGGCTCGA 506
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      82  G1yValCySserTyRleu 87
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      507  GGGGTGCTCTCTGCTT 524

RESULT 165
LOCUS       CV119018
DEFINITION  734 bp mRNA linear EST 30-AUG-2004
            AGENCOURT 31557860 NIH MGC 270 Rattus norvegicus cDNA clone
            IMAGE:7444574 5', mRNA sequence.
ACCESSION   CV119018

```


VERSION	CV119018.1	GI:51640419
KEYWORDS	EST.	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
	Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	1 (bases 1 to 734)	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Daniela S. Gerhard, Ph.D.	

Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.lln.gov>
Plate: LMNL5744 row: h column: 12
High quality sequence start: 18
High quality sequence stop: 735.
Location/Qualifiers
1. .734

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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/cclone="IMAGE:744574"
/tissue_type="whole placenta, 2 pooled"
/lab_host="DH10B Tona"
/cclone_lib="Nih_MGC_270"
/notes="Organ: Placenta; Vector: pExpress-1; Site_1: EcoRV
Site_2: NotI; Tissue was collected from two pooled
placentas from the 21st day of pregnancy, 1st strand cDNA
was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was cloned into the Not I and EcoRV
sites of pExpress-1. Library was size-selected for >1.25
kb fragments for an average insert size of 2.15 kb.
Library was normalized to Cot7. A non-normalized version
of this library is also available (Nih_MGC_269). Library
was constructed by Open Biosystems (Huntsville, AL). Note
this is a Mammalian Gene Collection library"

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ORIGIN	Alignment Scores	
Prad3 MO.:	2,878-16	Length: 734
Score:	210.50	Matches: 40
Percent Similarity:	67.4%	Conservative: 13
Best Local Similarity:	52.3%	Mismatch: 27
Query Match:	47.0%	Indels: 1
DB:	7	Gaps: 1

QY 2 GtUuRGAlAlAuAnsSerTyZpHeGluProProVaGlGluSerAlAluGluUaRGaRG 21
 Db 123 AAAAAAGGTTGAGCCCTTTCTTCAGAGGAGAGAAAGACCTTGCCGCGCTACACAG 182
 QY 22 ProGluThrIleSerGluProLyThrTyValAspLeuThAsnGluGluThrThaAp 41
 Db 183 CCTCGACATCTCCAAAGCCGAGACATGTGATCTAACCAAGAGAGATCCAAATGAT 242
 QY 42 SerThrIleSerLyrlleSerProSerGluAspPhdGlnGluAsnGlySerMetPhe 61
 Db 243 ACCACCATTTAAACACAGCTCACT---GGAATCCTCTGAAGAGATGACGACATATC 299
 QY 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaRG 81

Db	300	TCCTCATTACCTGGAATATGATGATTAGATGATGATCCAGAGAGGCGTGA	350
Qy	82	GIYVAIYSAEYRIYLU	87
Db	360	GGGGTGTGTTCTCGCCTT	377

RESULT 166	
CB545297	
LOCUS	CB545297
DEFINITION	639 bp mRNA linear EST 01-APR-2000
ACCESSION	AL080000:NR001-00108-F11-A nr001 (10855) Rattus norvegicus cDNA
VERSION	CB545297
KEYWORDS	CB545297.1 GI:29429238
SOURCE	EST.
ORGANISM	Rattus norvegicus (Norway rat)
	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 639)
AUTHORS	Amgen EST Program.
TITLE	Amgen Rat EST Program
JOURNAL	Unpublished (2003)
COMMENT	Contact: Dan Fitzpatrick

```

Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00108 row: f column: 11.
Location/Qualifiers
source 1. .639
FEATURES

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/morganism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nr01-00108-f11"
/cisue_type="Dorsal Root Ganglia"
/clone_lib="nr01 (10855)"
/notes="Vector: pSPOR1; Site_1: SalI; Site_2: NotI; rat
dorsal root ganglia"

ORIGIN

Alignment Scores:
Pred. No.:      7 76e-16      Length:      639
Score:          206.50      Matches:      44
Percent Similarity: 67.4%      Conservative: 14
Best Local Similarity: 51.2%      Mismatches:  27
Query Match:    46.1%      Indels:      1
DB:              6          Gaps:          1

US-10-757-745-2.COPY_54_140 (1-87) x CHS45297 (1-639)

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QY	2	GluArgAlaLeuAnsSerTyrPheGlnProValIguInuSerNlaLeuGluArg	21
Db	149	AAAAAGGGTTGAGCCCTCTTCATCGAGCAGAACAACCATCCAGCGGCCTCACCAAG	208
QY	22	ProGluThrIleSerGlnProLysThrTyrValAspLeuThrAngGluInuThrThrAsp	41
Db	209	CCTCGAGATCCCTCCCAAGTCCGAGAGACTATGTATTAACCAATAGAGATCAAAATAT	266
QY	42	SerThrThrSerLysIleSerProSerGluAspThrGlnGluAngLysSerMetPhe	61
Db	269	ACCACCACTATTAGAACCAAGTCCATCT---GGAACCTCCTCMAMAMATATGCGACCTATC	322
QY	62	SerLeuIleThrTyrPaniIleAspLIyleuAspLeuAsnAnuLeuSerGluArgIleArg	81
Db	326	TCTTTCATTTAGCTGGAGATAATTGATGATTAGATGATGCAATCTCCCAAGAGGGGCTGA	385
QY	82	GlyValCysSerTyrLeu	87
Db	386	GGGGTGTTCTCGCCTT	403
RESULT	167		
AL854676			
JOCUS			
	640 bp	mRNA	linear EST 02-DEC-2000

DEFINITION AL854676 XGC-egg Xenopus tropicalis cDNA clone TEG9019p19 5', mRNA sequence.

ACCESSION AL854676

VERSION AL854676.2 GI:38630173

KEYWORDS EST.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae; Xenopus; Silurana.

AUTHORS 1 (bases 1 to 640)

TITLE Croining M.D.R., Ashurst J.L., Taylor R., Zorn A.M. and Rogers J.

JOURNAL Sanger Xenopus tropicalis EST project 2001 (11.2003)

COMMENT Unpublished (2003)

On Sep 15, 2002 this sequence version replaced gi:22874895.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS_SEQUENCE_ID: TEG9019p19.plksp6

Sequencing primer: Sp6

This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

cDNA was oligo dt primed from 5ug of poly A+ RNA from egg

ECORI-NotI cut cDNA was then ligated into pCS107 with EcorI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcorI; Site 2: NotI

Host: Escherichia coli XL1-blue.

Location/Qualifiers

1..640

/organism="Xenopus tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="TEG9019p19"

/dev_stage="egg"

/lab_host="Escherichia coli XL1-blue"

/clone_lib="XGC-egg"

/note="Vector: pCS107; Site 1: EcorI; Site 2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from egg. EcorI-NotI cut cDNA was then ligated into pCS107 with EcorI at the 5' end and NotI at the 3' end"

ORIGIN

Alignment Scores:

Pred. No.: 3,93e-15 Length: 640

Score: 201.00 Matches: 44

Percent Similarity: 61.8% Conservative: 19

Best Local Similarity: 43.1% Mismatches: 21

Query Match: 44.9% Indels: 18

DB: 1 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) X AL854676 (1-640)

QY 1 MetGUARXAlaLeuSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20

DB 147 ATGGAAGGCGCAATTAATCTTTCTTGAGCCGCGGCGAGTCAGCTTGCAAAACAAA 206

QY 21 ATGPGGluThrIleSerGluPro-----Lys 29

DB 207 GCTGACGTGATATGACATCTTAAAGCAAGACTATGCTGGAACGCTCCGAT 266

QY 30 ThrTYRValAspLeuThrAsnGluGlu-----ThrThraSpSerThrThraSer 45

DB 267 TCATGTATTGACCTCACCGCGATGCTAGTGGTTACCAATCAAGAACCACTACACAC 326

QY 46 LysIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 65

DB 327 AAT-----TCTCCACACTGTGAGCAAGAGATGAGACATTTTCTTTCGACT 377

QY 66 TTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgIlyValCysSer 85

DB 378 TCGAATATATGATGCGCTTGATGAATCAATATGTCGAGAAAGGCTGCTGCTGTCTTCC 437

QY 86 Tyrlen 87

DB 438 TATTTG 443

RESULT 168

LOCUS CX958091

DEFINITION JGI CAAO9595.fwd NIH XGC tropfEs Xenopus tropicalis cDNA clone IMAGE:7706138 5', mRNA sequence.

ACCESSION CX958091

VERSION CX958091

KEYWORDS EST.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae; Xenopus; Silurana.

AUTHORS 1 (bases 1 to 842)

TITLE Richardson P., Lucas S., Rokhsar D., Dettler J.C., Ng D.C., Brokstein P. and Lindquist E.A.

JOURNAL DOE Joint Genome Institute Xenopus tropicalis EST project

COMMENT Unpublished (2004)

Other ESTs: JGI CAAO9595.rev

Contact: Lindquist, E.A., Richardson, P.

DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 296 5600

Fax: 925 296 5710

Email: cdna@jgi-psf.org

Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley)

http://tropicalis.berkeley.edu/home)

cDNA Library Preparation: DOE Joint Genome Institute

http://www.jgi.doe.gov

Clone Sequencing: DOE Joint Genome Institute; http://www.jgi.doe.gov

Clone Distribution: I.M.A.G.E. Consortium/LLNL

http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix 'fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.

Plate: CAAO 0097 row: f column: 24

High quality sequence scop: 821.

Location/Qualifiers

1..842

/organism="Xenopus tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="IMAGE:7706138"

/sex="male"

/tissue_type="Testes"

/dev_stage="Adult"

/lab_host="Electromax DH10B"

/clone_lib="NIH XGC tropfEs"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; This library was made from dt primed cDNA and cloned into Invitrogen pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTCTGATGCGAG CGGCGGCTTTTCTTTTCTTTT 3'. cDNA were ligated to SalI adapter (5' TCGACCCAGCGGCTCGG and 5'CGAGCGGCTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVSPORT6 vector."

ORIGIN

Alignment Scores:

Pred. No.: 5.63e-15 Length: 842

Score: 201.00 Matches: 44

Percent Similarity: 61.8% Conservative: 19

Best Local Similarity: 43.1% Mismatches: 21

Query Match: 44.9% Indels: 18

DB: 8 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x CX8358091 (1-842)

OY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 204 ATGGAAGGGCGATTATATCTTTCTTTGAGCTGGGGTGGAGCCCTTGCAAAACAA 263
OY 21 ArgProGluThrIleSerGluPro-----Lys 29
Db 264 GCTGACGCTGATATGACAGATCTTTAAAGCAGAGACTATGTCTGGAACCTCTCCGAT 323
OY 30 ThrTyrValAspLeuThrAsnGluGlu-----ThrThrAspSerThrThrSer 45
Db 324 TCATGTATTGACCTGACTGCGATGACTTACTGTTACCAAAATCAGAAACCACTACACG 383
OY 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
Db 384 AAC-----TCCCTCCACTGTGAGCAGACAGATAGAGCCATTCTTCTGTGACT 434
OY 66 TrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85
Db 435 TGGAAATATGATGAGCTTGATGATCAAAATGTCAGAAAGGGCTGTGTGTGTCC 494

OY 86 TyrLeu 87
Db 495 TATTGG 500

RESULT 169

CX843565 866 bp mRNA linear EST 02-FEB-2005
LOCUS JGI_CAK11139.Fwd NIH_XGC_tropBrn3 Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7661931 5', mRNA sequence.
ACCESSION CX843565
VERSION CX843565.1 GI:58497531
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 866)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI_CAK11139.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org

Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley)
http://tropicalis.berkeley.edu/home/
cDNA Library Preparation: DOE Joint Genome Institute
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute; http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI clone id and the direction of sequencing. The suffix ".fwd"
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CNAK 0117 row: e column: 1
High quality sequence stop: 795.

FEATURES

1..866
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7661931"
/tissue_type="Brain"

/dev_stage="Adult"
/lab_host="ElectroMAX DH10B"
/clone_lib="NIH_XGC_tropBrn3"
/note="Vector: pCMVSPORT6; Site 1: SalI, Site 2: NotI;
This library was made from dT primed cDNA and cloned into
Invitrogen pCMVSPORT6 vector. The work was done at DOE
Joint Genome Institute. Poly A RNA were primed with 3'
GACTAGTTCTTAGATCGGAG CGGCGCCCTTTTCTTTTCTTTT 3' cDNA
were ligated to SalI adapter (5' TCGACCAAGCTCGC and
5' CGACCGCTGG3), digested with NotI, size fractionated in
1.1% agarose gel electrophoresis and ligated into NotI and
SalI digested pCMVSPORT6 vector."

ORIGIN

Alignment Scores:
Pred. No.: 5,846-15 Length: 866
Score: 201.00 Matches: 44
Percent Similarity: 61.84 Conservative: 29
Best Local Similarity: 43.14 Mismatches: 21
Query Match: 44.94 Indels: 18
Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x CX843565 (1-866)

OY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 207 ATGGAAGGGCGATTATATCTTTCTTTGAGCTGGGGTGGAGCCCTTGCAAAACAA 266
OY 21 ArgProGluThrIleSerGluPro-----Lys 29
Db 267 GCTGACGCTGATATGACAGATCTTTAAAGCAGAGACTATGTCTGGAACCTCTCCGAT 326
OY 30 ThrTyrValAspLeuThrAsnGluGlu-----ThrThrAspSerThrThrSer 45
Db 327 TCATGTATTGACCTGACTGCGGATGACTTACTGTTACCAAAATCAGAAACCACTACACG 386
OY 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
Db 387 AAT-----TCCCTCCACTGTGAGCAGACAGATAGAGCCATTCTTCTGTGACT 437
OY 66 TrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85
Db 438 TGGAAATATGATGAGCTTGATGATCAAAATGTCAGAAAGGGCTGTGTGTGTCC 497

OY 86 TyrLeu 87
Db 498 TATTGG 503

RESULT 170

CX824886 879 bp mRNA linear EST 01-FEB-2005
LOCUS JGI_CAK4320.Fwd NIH_XGC_tropBrn3 Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7655281 5', mRNA sequence.
ACCESSION CX824886
VERSION CX824886.1 GI:58402449
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 879)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI_CAK4320.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley):
<http://tropicalis.berkeley.edu/home>
 CDNA Library Preparation: DOE Joint Genome Institute:
<http://www.jgi.doe.gov>
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LNL:
<http://image.llnl.gov>
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone ID and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: CAK 0045 row: 0 column: 23
 High quality sequence stop: 779.

FEATURES

Source

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1. 879
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7655281"
/cisue_type="Brain"
/dev_stage="Adult"
/lab_host="Electromax DH10B"
/clone_lib="NIH XGC trophoblast"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; This library was made from DT primed cDNA and cloned into Invitrogen pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTGTTCTGATGCGAG CGAGCGCCCTTTTCTTTTCTTTT 3'. cDNA were ligated to SalI adapter (5' TCGACCGACGCTCGG and 5'CGAGCGCTGCGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVSPORT6 vector."

```

ORIGIN

Alignment Scores:

Pred. No.:	5,966-15	Length:	879
Score:	201.00	Matches:	44
Percent Similarity:	61.8%	Conservative:	19
Best Local Similarity:	43.1%	Mismatches:	21
Query Match:	44.9%	Indels:	18
	8	Gaps:	3

US-10-757-745-2_COPY_54_140 (1-87) x CK824886 (1-879)

```

OY 1 MetGUATGAlaLeuAmsSerTyRheGluProProValGluGluSerAlaLeuGluArg 20
Db 204 ATGGAAGGGCGATTAATCTTTCTTTGAGCTGGGCGAGTCAAGCTTGCAAAACAA 263
OY 21 ArgProGluThrIleSerGluPro-----Lys 29
Db 264 GCTGAGCTGATATGAGATCTTTAAAGCAAGACTAGTCTGAACTGCTTCGAT 323
OY 30 ThrTyValAspLeuThrAsnGluGlu-----ThrThrAspSerThrThrSer 45
Db 324 TCATGTATATGACCTTACCGGCGATGACTTACCAATCGAAGCAATCTCCAGC 383
OY 46 LysIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 65
Db 384 AAT-----TCTTCCACTGTGAAGCAAGAGATGAGCCATTTTCTTCTGACT 434
OY 66 TTPAenlleaSPGLyleuAspLeuAmsSerGluArgAlaArgGluValaGlySer 85
Db 435 TGGATATATGATGGCTTGATCAATCAATGTGCGAAGAGGCTGTGTGTGTTC 494
OY 86 Tytleu 87
Db 495 TATTGT 500

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RESULT 171
 LOCUS BB609556 712 bp mRNA linear EST 26-OCT-2001
 DEFINITION BB609556 RIKEN full-length enriched, 18 days embryo Mus musculus

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

CDNA clone 1110007K13 5', mRNA sequence.
 BB609556
 BB609556.1 GI:16451282
 EST.
 Mus musculus (house mouse)
 Mus musculus

REFERENCE AUTHORS

Bukacinska, Metaxas, Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 712)

TITLE JOURNAL COMMENT

Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichipillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yamakawa, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.

FEATURES source

```

1. 712
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="1110007K13"
/dev_stage="18 days embryo"
/lab_host="SOLR"
/note="RIKEN full-length enriched, 18 days embryo"
/note="Site 1: XhoI; Site 2: SacI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGCGGCGGCGGCTGAGTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'

```

ORIGIN

GAGAGAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCCCCCCCC 3'1.
CDNA was cleaved with XhoI and SefI."

Alignment Scores:

Pred. No.: 7.03e-15 Length: 712
Score: 199.50 Matches: 43
Percent Similarity: 65.14 Conservative: 13
Best Local Similarity: 50.04 Mismatches: 29
Query Match: 44.54 Indels: 1
DB: 2 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BB609556 (1-712)

QY 2 GUUAGAlaleuanserTYrPhgIuProProValGluGluSerAlaleuGluArg 21
Db 260 CAGAAAGCCCTGAGCGCTTCTGAGCTCCAGAGAACGACCAAGGCTGCGCCGAC 319
QY 22 ProGluThrlleSerGluProlyeThrTYrValAspLeuThraSmGluGluThrThra 41
Db 320 CCTCCAGCTCTTCAGAGCTCCAGAGCTTATGATCTTACCAAGAGATGCAATGAT 379
QY 42 SerThrThrlleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGlnGln 61
Db 380 ACAACCATTTTGAAGCCAGTCATCT--GGAACCTCTCTAGAAAGATGACGACTATT 436
QY 62 SerleuIleThrTYrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 81
Db 437 TCTTCAATTAAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 496
QY 82 GlyValCysSerTyrLeu 87
Db 497 GAGGTGTCTCTGCTTA 514

RESULT 172

CD699206 274 bp mRNA linear EST 25-JUN-2003
LOCUS EST15729 human nasopharynx Homo sapiens CDNA, mRNA sequence.
DEFINITION CD699206
ACCESSION CD699206
VERSION CD699206.1 GI:32228261
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 274)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)

TITLE

JOURNAL
COMMENT

FEATURES

1..274
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="human nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Alignment Scores:

Pred. No.: 2.33e-15 Length: 274
Score: 199.00 Matches: 44
Percent Similarity: 95.94 Conservative: 3

Best Local Similarity: 89.84 Mismatches: 0
Query Match: 44.44 Indels: 2
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CD699206 (1-274)

QY 2 GUUAGAlaleuanserTYrPhgIuProProValGluGluSerAlaleuGluArg 21
Db 130 CAGAGGCTCTGAGCTCTTCTGAGCTCCAGAGAACGACCAAGGCTGCGCCGAC 189
QY 21 GProGluThrlleSerGluProlyeThrTYrValAspLeuThraSmGluGluThrThra 41
Db 190 ACTGAAACATCTCTGAGCCCAAGCCTATGACTTAACCAAGTGAAGAAACAATG 249
QY 41 spSerThrThrlleSer 48
Db 250 ATTCACCATCTTAATATCAGC 272

RESULT 173

CB728877 475 bp mRNA linear EST 11-APR-2003
LOCUS AMGNNUC:CB728877-00016-D12-A Colon rat 3 (10415) Rattus norvegicus CDNA
DEFINITION CB728877-00016-D12-A, mRNA sequence.
ACCESSION CB728877.1 GI:29796001
VERSION CB728877.1
KEYWORDS EST.

SOURCE

ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 475)
Amgen EST Program
Amgen Rat EST Program
Unpublished (2003)

JOURNAL

COMMENT

CONTACT

AMGEN, INC

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00016 row: d column: 12.

Location/Qualifiers

1..475
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone_lib="Colon rat 3 (10415)"
/clone_lib="Colon rat 3 (10415)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Colon
rat 3 fetal rat intestine"

ORIGIN

Alignment Scores:

Pred. No.: 5.55e-15 Length: 475
Score: 198.50 Matches: 43
Percent Similarity: 65.14 Conservative: 13
Best Local Similarity: 50.04 Mismatches: 29
Query Match: 44.14 Indels: 1
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x CB728877 (1-475)

QY 2 GUUAGAlaleuanserTYrPhgIuProProValGluGluSerAlaleuGluArg 21
Db 216 AAAAAAGCTTGAAGCTCTTCTGAGAGCCAGAGACGACCTAGCGGCTTACACAG 275
QY 22 ProGluThrlleSerGluProlyeThrTYrValAspLeuThraSmGluGluThrThra 41
Db 276 CCTCCAGACCTCCAGAGCTCCAGAGCTTATGATGATGATGATGATGATGATGATGAT 335
QY 42 SerThrThrlleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGlnGln 61
Db 336 ACAACCATTTTGAAGCCAGTCATCT--GGAACCTCTCTAGAAAGATGACGACTATC 392

AL5858410 LOCUS DEFINITION AL5858410 634 bp mRNA EST 02-DEC-2003
AL5858410 XGC-egg Xenopus tropicalis cDNA clone TBSg059p03 5'-UTR mRNA
sequence.
AL5858410
AL5858410.2 GI:38633375
EST.
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 634)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22878591.
COMMENT
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TBSg059p03.p1ksr6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with ECORI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site 2: NotI
Host: Escherichia coli XL1-blue.
FEATURES
Source
1..634
Location/Qualifiers

```

/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEgg059p03"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_id="XGC-egg"
/notes="Vector: PCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into PCS107 with
EcoRI at the 5' end and NotI at the 3' end"

```

ORIGIN

Alignment Scores:

Pred. No.:	5.5e-14	Length:	634
Score:	192.00	Matches:	42
Percent Similarity:	60.8%	Conservative:	20
Best Local Similarity:	41.2%	Mismatches:	22
Query Match:	42.9%	Indels:	18
DB:	1	Gaps:	3

US-10-757-745-2_COPY_54_140 (1-87) X AL858410 (1-634)

```

Oy      1  MetcIuArgAlaLeuAenSerTyRPhaGluProProValGluIuSerAlaLeuGluA 20
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      127 GTTCGGAGGGCGAGTATATCTCTTCTTGACCCCTGGGTGGAGTCACCCCTTGCAAAACAA 18
Oy      21 ArgProGluThrIleSerGluPro-----Lys 29
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      187 GCTGCACGCTGATATAGCAGATCCTTTAAACAGAGCATATGCTGAACTGTTCCGAT 24
Oy      30 ThrTyValAspLeuThrAngGluGlu-----ThrRapSerThrRpsar 45
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      247 TCATGTAATGACCTCACCGGCGAGTACTTGAGTTACCAATCAAGACCACTACAC 30
Oy      46 LysIleSerProSerGluAspThrGlnGluAsnGlySerMetPheSerLeuIleThr 65
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      307 AAT-----TCCTCCACTGTGAGACAGAAAGATGAGGCCATTTTCTTTCTGACT 35
Oy      66 TrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85

```

DB	QY	DB
358	TGGATATAGATGGCTTGATGAAATCAATGTCGAGAAAGGCGTCGTGTGTGTCC	417
86	TyrLeu	87
418	TAATTG	423

RESULT	178				
AL901140					
LOCUS	AL901140	638 bp	mRNA	linear	EST 04-DEC-2003
DEFINITION	AL901140 XGC-egg <i>Xenopus tropicalis</i> cDNA clone TEG907704 5', mRNA sequence.				
ACCESSION	AL901140				
VERSION	AL901140.2				
KEYWORDS	GI:38699862				
SOURCE	EST.				
ORGANISM	<i>Xenopus tropicalis</i> (western clawed frog)				
	<i>Xenopus tropicalis</i>				

This sequence is from a *Xenopus* gene Collection (XGC) library constructed by Aaron M. Zorn. cDNA was oligo dt primed from 5ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end. Vector: pCS107; Site_1: EcoRI; Site_2: NotI Host: *Escherichia coli* XL1-blue. Location/Qualifiers

FEATURES

```

/lab_host="Escherichia coli XL1-blue"
/clone_1lb="xgc-eggs"
/notes="vector: pCS107, Site_1: EcoRI, Site_2: NotI, cDNA
was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

```

Alignment Scores:

Score:	192.00	Matches:	42
Percent Similarity:	60.8%	Conservative:	20
Best Local Similarity:	41.2%	Mismatches:	22
Query Match:	42.9%	Indels:	18
DB:	1	Gaps:	3

US-10-757-745-2_COPY_54_140 (1-87) × AL901140 (1-638)

QY	1	MercGluArgAlaLeuGlnSerSerTyrrPheGluProProValGluGluSerAlaLeuGluArg	20
DB	2	GHTGGAGGGCGATTATTCCTTCTTGTGAGCCCTGGGGTGAATCAGCCTTGCAAAAACAA	61
QY	21	ArgProGluThrThrIleSerGluPro-----Lys	29
DB	62	GCAGCAGCGATATACAGATCCTTTAAAGCAAGACATATGTCGAACCTCCCAT	12

Pred. No.:	1,85e-13	Length:	816
Score:	189.00	Matches:	42
Percent Similarity:	63.0%	Conservative:	21
Best Local Similarity:	42.0%	Mismatches:	23
Query Match:	42.2%	Indels:	14
DB:	7	Gaps:	4

```

Oy      1  MetG1AArgAlaIeuuanserTyzHeG1uPProPovaG1uGluSerAlaIeuG1uArg 20
Db      227  ATGGAAAGGCGACATCTTACTTTAGAGCTGGCGTG--GAGTGCACCTTACAAAC 283
Oy      21  ArgProG1uThr---IleSerG1uPro-----Lys 29
Db      284  AAACTCGCAGCGATCTACAGACCCCTTTAAAGCAAGATGATGCATGACTTACTCTGAC 343
Oy      30  ThrTyValasPleuThraNsngluG1uThrThraPseSerThrIserLyIleSerPro 49
Db      344  GCAATGATTGACTTGACTAGCGATACCTTGGTGGCTACCAATAGAAAGCTTTACACAGC 403
Oy      50  SerG1uAspThr-----GlnG1uInluAnsnglySerMetPseIserLeuIethrTrpAsn 67
Db      404  AACTCTCTACTGTGAAACAACAAGAATAGAGCCATTTTACTCTTTCACTGGAAT 465

```

```

Oy 68 ILASGSLVleuaspneumnsamnsbergiurigaiaargciyValCysserTleu 87
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 464 ATGATGCGCTTGAATGAATCAACCTTGCAGAGAGCGCTCGTGGCTATATGTTCTGTTG 523

```

ACCESSION IMAGE:720513.4 5', mRNA sequence.
VERSION CK798287
KEYWORDS CK798287.1 GI:42810283
SOURCE EST.
Xenopus laevis (African clawed frog)

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
<i>Xenopus laevis</i> Bukaryova, Merliza Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae, Pipidae; Xenopodinae; Xenopus; Xenopus. 1 (bases 1 to 876) NIH-MGC http://mgc.ncl.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgabds-remail.nih.gov Tissue Procurement: Igor B. Dawid					

```

FEATURES
    source
        cdna Library Preparation: Express Genomics
        cdna Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
        DNA Sequencing by: Agencourt Bioscience Corporation
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LINTL at:
        http://image.llnl.gov
        plate: LLAM15085 row: k column: 20
        High quality sequence stop: 650.
        location/Qualifiers
            1..876
            /organism="Xenopus laevis"
            /mol_type="mRNA"
            /db_xref="taxon:8355"
            /clone_image="7205134"
            /issue_type="Pooled samples from 6 adult male testis"
            /lab_host="DH10B Tona"
            /clone_1lb="NICHD XGC Te2N"
            /notes="Organ: testis; Vector: pExpress-1; Site:1: EcorV;
            Site 2: NotI; RNA obtained from 6 adult male testis. CDNA"

```

5'-pGACTAGTCTAGATCGGAGCGGCCCC (T)_{25-3'} and cloned into

ORIGIN

the Ecore/NorI sites of pXpress-1. Size-selection >1kb resulted in an average insert size of 1.15 kb. This primary, microquantity library is normalized to Cots (non-normalized primary library is NICHG XGC Fe2) and was constructed by Express Genomics (Frederick, MD). Note: this is an NIH_XGC library"

Alignment Scores:

Pred. No.: 2.03e-13 Length: 876
Score: 189.00 Matches: 42
Percent Similarity: 63.0% Conservative: 21
Best Local Similarity: 42.0% Mismatches: 23
Query Match: 42.2% Indels: 14
DB: 7 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x CK798287 (1-876)

QY 1 MetGUATGAlaLeuAnSerTYrPheGluProValGluGluSerAlaLeuGluArg 20
DB 207 ATGGAAAGGGCGATCAATCTTACTTGGAGCTGGGGTG--GAGTCGACCTTACAAAC 263
QY 21 ArgProGluThr--IleSerGluPro-----Lys 29
DB 264 AAACCTGACGCTGATCTAGACAGACCTTAAAGCAAGATGATGACGATTAACCTTGAC 323
QY 30 ThrTYrValaLeuThrAnGluGluThrThraPseThrThrSerLysIleSerPro 49
DB 324 GCATGATTGACTTGAAGCTAGCGATGCTGGGCTCAACATCAAGAGCTTACACAGC 383
QY 50 SerGluAsePThr-----GlnGlnGluAnGlySerMetPheSerLeuIleThrTyrAsn 67
DB 384 AACCTCCTACTGTGAACAACAAGAGATGAGAGCCATTTTACCTTCTTACATGAGAT 443
QY 68 IleAseGlyLeuAsePLeuAnAsePLeuSerGluValaGlyValCysSerTYrLeu 87
DB 444 ATGATGGCGCTTGATGATCAACAGTTGCAAGAGGGCTCGTGTGATTTCTCTTTG 503

RESULT 183

CA972607 927 bp mRNA linear EST 27-FEB-2003
LOCUS AGENCOURT 10766356 Wellcome CRC psk egg Xenopus laevis cdna clone
DEFINITION IMAGE:632452 5', mRNA sequence.
ACCESSION CA972607
VERSION CA972607.1 GI:27505261
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE

AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Journal Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaapb@remail.nih.gov
Tissue Procurement: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)
CDNA Library Preparation: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL3768 Row: d Column: 21
High quality sequence start: 8
Location/Qualifiers
1 927
/organism="Xenopus laevis"

FEATURES

source

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6324452"
/cisseq_type="egg"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="Wellcome CRC psk egg"
/note="Vector: pBluescript SK-; Site 1: NotI, Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Library was constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute).
Note: This is a Xenopus Gene Collection (XGC) library."

Alignment Scores:

Pred. No.: 2.19e-13 Length: 927
Score: 189.00 Matches: 42
Percent Similarity: 63.0% Conservative: 21
Best Local Similarity: 42.0% Mismatches: 23
Query Match: 42.2% Indels: 14
DB: 6 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x CA972607 (1-927)

QY 1 MetGUATGAlaLeuAnSerTYrPheGluProValGluGluSerAlaLeuGluArg 20
DB 209 ATGGAAAGGGCGATCAATCTTACTTGGAGCTGGGGTG--GAGTCGACCTTACAAAC 265
QY 21 ArgProGluThr--IleSerGluPro-----Lys 29
DB 266 AAACCTGACGCTGATCTAGACAGACCTTAAAGCAAGATGATGACGATTAACCTTGAC 325
QY 30 ThrTYrValaLeuThrAnGluGluThrThraPseThrThrSerLysIleSerPro 49
DB 326 GCATGATTGACTTGAAGCTAGCGATGCTGGGCTCAACATCAAGAGCTTACACAGC 385
QY 50 SerGluAsePThr-----GlnGlnGluAnGlySerMetPheSerLeuIleThrTyrAsn 67
DB 386 AACCTCCTACTGTGAACAACAAGAGATGAGAGCCATTTTACCTTCTTACATGAGAT 445
QY 68 IleAseGlyLeuAsePLeuAnAsePLeuSerGluValaGlyValCysSerTYrLeu 87
DB 446 ATGATGGCGCTTGATGATCAACAGTTGCAAGAGGGCTCGTGTGATTTCTCTTTG 505

RESULT 184

BB867803 519 bp mRNA linear EST 09-JUN-2003
LOCUS BB867803
DEFINITION BB867803 RIKEN full-length enriched, B cells CRL-1669 BCL1 Clone
13-20-183 CDNA Mus musculus CDNA clone G4D0010624 5', mRNA
sequence.
ACCESSION BB867803
VERSION BB867803.1 GI:17114013
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Eucarchontoglires; Glires; Rodentia;
Sciurognathu; Muridae; Murinae; Murinae; Mus.

REFERENCE

AUTHORS Akimura, Y., Akimura, T., Carninci, P., Furuno, M., Hanganaki, T., Hayashida, Y., Hiramoto, K., Hirose, T., Hirazaki, T., Imachi, K., Ishii, Y., Ito, M., Kawai, J., Kohjima, Y., Komuro, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, E., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyu, T., Watanabe, Y., Yasunishi, A., Yurimatsu, M., and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2003)
Unpublished (2001)

JOURNAL

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

TITLE
McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C., Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Lauder, V., Schachter, V., Queller, F., Sautin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J., and Roost Croallius, H.
Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype

JOURNAL
Nature 431 (7011), 946-957 (2004)

REFERENCE
15496914

AUTHORS
2 (bases 1 to 718)

JOURNAL
Submitted (25-NOV-2004) Genoscope - Centre National de Sequencage - 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr Web : www.genoscope.cns.fr) On Dec 3, 2004 this sequence version replaced g1:51135613.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.

FEATURES
Location/Qualifiers
1..718
/organism="Tetraodon nigroviridis"
/mol_type="mRNA"
/db_xref="taxon:99883"
/tissue_type="liver"

ORIGIN

Alignment Scores:
Pred. No.: 1.43e-12 Length: 718
Score: 181.50 Matches: 43
Percent Similarity: 57.0% Conservative: 14
Best Local Similarity: 43.0% Mismatches: 22
Query Match: 40.5% Indels: 21
Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x CNS05S5I (1-718)

QY 1 MetGUARGAlaleuanserTyrPheGluProProvalGluGlu---SeralaleGlu 19
DB 160 ATGGAGAGAGCTCTTAATCTCTTTGACACTGAATGAAGAAAGTGTGGAGTAGAA 219
QY 20 ATGAGPProGluThrIleSer-----Glu 27
DB 220 AATTCGCCAGAGACGAATCTCTGTCCAAACAAACGACAGAGTAGAGCAATCT 279
QY 28 ProLysrThrValAspLeuThrAsnGluGluThrThrAspSerThrSerLys 47
DB 280 CCAGCGGCTGTATAGATTGACTGAA-----GACAGTCTGCATCTTCAGAC 327
QY 48 SerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrp 67
DB 328 AAACCGTCGAAGATGATGACCAAG-----CTTTCGCTGATTAACCTTGGAAC 375
QY 68 IleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
DB 376 GTGGATGAGACTGATGCCACCAACCTAGCTGAACGCCAGCGCTGTCTTTATT 435

RESULT 188
DN851694 463 bp mRNA linear EST 20-APR-2005
LOCUS 4147331 BARC 3GAL chicken mixed tissue Gallus gallus cDNA clone
DEFINITION 3GAL 45109 5', mRNA sequence.
ACCESSION DN851694
VERSION DN851694.1 GI:62810854
KEYWORDS EST.
SOURCE Gallus gallus (chicken).
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 463)
AUTHORS Evock-Clover, C.M., Ashwell, C.M., McMurtry, J.P., Lillehoj, H.S., Matukumalli, L.K. and Van Tassel, C.P.

TITLE
Characterization of expressed sequence tags generated from multiple chicken tissues

JOURNAL
Unpublished (2004)

COMMENT
Contact: Christina M. Clover
Growth Biology Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm215 BARC-East, Beltsville, MD 20705, USA
Tel: 3015048224
Fax: 3015048623
Email: chris@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt '-' -trim fasta. Vector identified by cross match using options -mismatch 12 -mincore 18
Plate: 45 row: I column: 09
Seq primer: CCCAGTCACGACGTGTGTAACG
High quality sequence stop: 463.

FEATURES
Location/Qualifiers
1..463
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Leghorn and broiler"
/db_xref="taxon:9031"
/clone="3GAL 45109"
/lab_host="vDHSalpa"
/clone_id="BARC 3GAL chicken mixed tissue"
/note="Vector: pBluescript, SK+, Stragene, Site 1: NotI, Site 2: EcoRI, Normalized library of pooled RNA isolated from whole brain, ultimobranchial gland, parathyroid gland, cecal tonsil and primordial germ cells Multiple"

ORIGIN

Alignment Scores:
Pred. No.: 9.3e-13 Length: 463
Score: 181.00 Matches: 36
Percent Similarity: 76.7% Conservative: 10
Best Local Similarity: 60.0% Mismatches: 12
Query Match: 40.4% Indels: 2
Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x DN851694 (1-463)

QY 28 ProLysrThrValAspLeuThrAsnGluGluThrThrAspSerThrSerLys 47
DB 59 CCTGAGAGCTGTATGACTTCACAGCATGTGATCTGCAATTAACGACGAC----- 112
QY 48 SerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrp 67
DB 113 AGTGGTGCACTCCACAGACATGATGACAGAGGAGGAGGAGGAGGAGGAGGAG 172
QY 68 IleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
DB 173 ATGTATGGGCTGGACCTGGGAGATCTGACAGGACGAGGAGGAGGAGGAGGAG 232

RESULT 189
CX937111 782 bp mRNA linear EST 07-FEB-2005
LOCUS UGI_CMA05295.fwd NIH_XGC_tropics Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7702086 5', mRNA sequence.
ACCESSION CX937111
VERSION CX937111.1 GI:58726869
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 782)
AUTHORS Richardson, P., Lucas, S., Rokhsar, D., Deter, J.C., Ng, D.C., Brockstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: UGI_CMA05295.rev
Contact: Lindquist, E.A., Richardson, P.

DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley:
http://tropicalis.berkeley.edu/home)
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone ID and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Small Insert: Based upon one or more sequencing reads of this clone
where vector sequence was present at both ends, this clone has been
determined to contain a cDNA insert on the order of 600-1000 bases.
Plate: CNAO 0053 row: n column: 4
High quality sequence stop: 778.
Location/Qualifiers
1. 782
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7702086"
/sex="male"
/tissue_type="Testes"
/dev_stage="Adult"
/lab_host="NIH XCC Croptres"
/clone_lib="NIH XCC Croptres"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into
in vitro transcribed vector. The work was done at DOE
Joint Genome Institute. Poly A RNA was primed with 5'
GACTAGTCTAATGTCGCG CGCGCGCTTTTCTTTTCTT 3'. cDNA
were ligated to SalI adapter (5' TCAGCCACGCGTCGCG
5' CGAGCGCTGCG), digested with NotI, size fractionated in
1.1% agarose gel electrophoresis and ligated into NotI and
SalI digested PCMVSPORT6 vector."

FEATURES
source
1. 782
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7702086"
/sex="male"
/tissue_type="Testes"
/dev_stage="Adult"
/lab_host="NIH XCC Croptres"
/clone_lib="NIH XCC Croptres"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into
in vitro transcribed vector. The work was done at DOE
Joint Genome Institute. Poly A RNA was primed with 5'
GACTAGTCTAATGTCGCG CGCGCGCTTTTCTTTTCTT 3'. cDNA
were ligated to SalI adapter (5' TCAGCCACGCGTCGCG
5' CGAGCGCTGCG), digested with NotI, size fractionated in
1.1% agarose gel electrophoresis and ligated into NotI and
SalI digested PCMVSPORT6 vector."

ORIGIN

Alignment Scores:
Pred. No.: 1.85e-12 Length: 782
Score: 181.00 Matches: 42
Percent Similarity: 61.2% Conservative: 21
Best Local Similarity: 40.8% Mismatches: 21
Query Match: 40.4% Indels: 19
DB: 8 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x CX3937111 (1-782)

QY 1 MetGluArgAlaLeuAnuSerTyrPheGluProProValGluInuSeraAlaLeuGlu-Ar 20
Db 5 GTTCGAGAGCGGATTAATCTTTCTTTAGCGCTGCGGAGTCACTTTGCAAAACAA 64
QY 20 GARGProGluThrIleSerGluPro-----Ly 29
Db 65 AGCTGCAGCTGATATACAGATCTTTAAAGCAAGAGACTATGCTGGAACCTGTTCCGA 124
QY 29 eThrTyrValAspLeuThrAsnGluInu-----ThrThraspSerThrThrse 45
Db 125 TTCATGATTTACTGCTGCTGCGATGACTTAAGTTACCAATCAGAACTATCCGAG 184
QY 45 rlyserIleSerProSerGluAspThrGluInuGluAsnGlySerSerPheSerLeuIleTh 65
Db 185 CAAC-----TCCTCCACTGTGAAGCAAGAGATGAGCCATTTTCTCTTCTGAC 235
QY 65 rThrasnIleAspGlyLeuAspLeuAsnAsnSerGluArgAlaArgGlyValCyse 85
Db 236 TTGGAATATAGATGCGCTTATGATCAAAATGTCGACAGAAAGGCGCTGTGTGTGTTTC 295

QY 85 rTyrlen 87
Db 296 CTAATTG 302
RESULT 190
EX306203
LOCUS
DEFINITION
EX306203 tccay Oncorhynchus mykiss cDNA clone tccay0015b.c.23 5prim,
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 736)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29586848.
Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenaspport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0015 row: c column: 23
Seq primer: M13R.
Location/Qualifiers
1. 736
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tccay0015b.c.23"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tccay"
/note="Vector: pT73D-pac; Rainbow trout multi-clones -
normalized + 1 subtraction (tccay); Clone distribution:
AGENAS Resource Centre, Francois PUMET,
Francois.Pumet@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (URG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

FEATURES
source
1. 736
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tccay0015b.c.23"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tccay"
/note="Vector: pT73D-pac; Rainbow trout multi-clones -
normalized + 1 subtraction (tccay); Clone distribution:
AGENAS Resource Centre, Francois PUMET,
Francois.Pumet@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (URG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Alignment Scores:
Pred. No.: 2.66e-12 Length: 736
Score: 179.50 Matches: 45
Percent Similarity: 53.4% Conservative: 17
Best Local Similarity: 38.8% Mismatches: 25
Query Match: 40.1% Indels: 29
DB: 5 Gaps: 5
US-10-757-745-2_COPY_54_140 (1-87) x BX306203 (1-736)

QY 1 MetGluArgAlaLeuAnuSerTyrPheGluProProValGluInu---SeraAlaLeuGlu 19
Db 145 ATGAGAGAGAGCTGGAACATCTTTTCAGAGCTGACATGAGGACGTTTTCACACTGGA 204
QY 20 ArgArgPro---GluThrIleSerGluProGlyThr----- 30
Db 205 GATTCACCAAGAGAGACATCAGCCCTTAAGTTAAAGACGGAATTGACAAACCA 264

Oy		32	ValAspleurhxaengnugiutnrThraapSeThrthsSerlysiIeSerProScglu	51
Dd		324	GTTGACCTTAACAATGAAGAAACAACGTATTCCACCCTTAAAATCAGCCCAATCGAA	383
Oy		52	AspThgIngnlguabengiYseMetPhe-SerleuIIethrTrpaanilaepgiyle	71
Dd		384	GATTCAGCACAGAATAATGCAGCATGTTCTCTCTCATTAACCGAATATGTGATTT	443
Oy	71 u 71			
Dd	444 A 444			
RESULT 192				
LOCUS	B1444674			
DEFINITION	B1444674	581 bp	mRNA	linear EST 21-AUG-2001
KEYWORDS	de27d10.y3 Wellcome CRC PRN3 oocyte Xenopus laevis cDNA clone			
ACCESSION	IMAGE:3472962.5.	similar to TR:O95551 O95551 D3JOM3.3 ;,	mRNA	sequence.
VERSION	B1444674			
SOURCE	B1444674.1	GI:15269381		
ORGANISM	Xenopus laevis (African clawed frog)			
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Anphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;			
TITLE	Xenopodinae; Xenopus; Xenopus.			
JOURNAL	1 (bases 1 to 581)			
COMMENT	Cifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R. Washu Xenopus EST project. 1999 Unpublished (1999) Contact: Sandy Cifton, Ph.D. Washu Xenopus EST project, 1999 Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LNL at: info@image.jiml.gov High quality sequence stop: 403. Location/Qualifiers			
FEATURES	1..581			
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	/mol_type="mRNA"			
	/db_xref="taxon:8335"			
	/clone="IMAGE:3472962"			
	/tissue_type="oocyte"			
	/lab_host="DH10B (phage-resistant)"			
	/clone_lib="Wellcome CRC PRN3 oocyte"			
	/notes="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; CDNAS were oligo-dT primed and directionally cloned. Stegung according to Neuwook and Faber. Library was constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)." "			
ORIGIN				
Alignment Scores:	2.26e-12	length:	581	
Pred. No.:	179.00	Matches:	40	
Score:	62.2%	Conservative:	21	
Percent Similarity:	40.8%	Mismatches:	23	
Best Local Similarity:	40.0%	Indels:	14	
Query Match:		Gaps:	4	
DB:	3			
US-10-757-745-2_COPY_54_140 (1-87) x B1444674 (1-581)				

Qy 3 ArgAlaLeuAenSerTyPheGluProValGluGluSerAlaLeuGluArgPro 22
Db 30 AGGGCATCAATCTTACTTGAGACCTGGGGTG---GAGTCGACCTTCAAAACCAACT 86
Qy 23 GluThr---lIseGluPro-----LysThrTyr 31
Db 87 GCAGCTGATCTAGCAGACCTTTAAAGCAGAGATGACATGCACTTACCTGACGATCT 146
Qy 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
Db 147 ATTGACTTGACTAGCGATGACTGTGGCTCAACATACAGAGCTGTTACCAACCACTCC 206
Qy 52 AspThr-----GlnGlnGluAsnGlySerMetPheSerLeuIleThrTyrPheAsnIleAsp 69
Db 207 TCTACTGTGAACCAACAGAGATGAGACCATTTTACCTTTTACATGGAATATAGAT 266
Qy 70 GlyLeuAspLeuAenAenLeuSerGluArgAlaArgGlyValCysSerTyrlen 87
Db 267 GGCTTGATGATCAACAGCTTGACAGAGGGCTCGTGTATGTTCTGTGTTG 320

RESULT 193
LOCUS BE189858 688 bp mRNA linear EST 07-AUG-2000
DEFINITION db61e10.y1 Wellcome CRC psk egg xenopus laevis cDNA clone
IMAGE:3377514 5' similar to TR:095551 095551 DJ30M3.3 ;, mRNA
sequence.
ACCESSION BE189858
VERSION BE189858.2 GI:9729569
KEYWORDS EST.
SOURCE xenopus laevis (African clawed frog)
ORGANISM xenopus laevis

REFERENCE
AUTHORS Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 688)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
Pape,D., Martin,J., Wyllie,T., Underwood,K., Theisler,B., Bowers,Y.,
Person,B., Gibbons,M., Harvey,N., Rilter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
On Jun 22, 2000 this sequence version replaced gi:8668741.
Other ESTs: db61e10.x1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute). DNA sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/UMW at: info@image.1iml.gov
Seq primer: -40bp from GIBCO at: info@image.1iml.gov
High quality sequence step: 487.
Location/Qualifiers

FEATURES

source

1..688
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:3377514"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC psk egg"
/note="Vector: pBlueScript SK-; Site 1: NotI; Site 2:
EcoRI; cDNAs were oligo-dT primed and directionally
cloned. Library was constructed by N. Garrett, P. Lemaire,
A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute).
Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN

..C

Alignment Scores:

Pred. No.: 2,82e-12 Length: 688
Score: 179.00 Matches: 40
Percent Similarity: 62.24 Conservative: 21
Best Local Similarity: 40.84 Mismatches: 23
Query Match: 40.04 Indels: 14
DB: 2 Gaps: 4

US-10-757-745-2_copy_54_140 (1-87) x BE189858 (1-688)

Qy 3 ArgAlaLeuAenSerTyPheGluProValGluGluSerAlaLeuGluArgPro 22
Db 23 AGGGCATCAATCTTACTTGAGACCTGGGGTG---GAGTCGACCTTCAAAACCAACT 79
Qy 23 GluThr---lIseGluPro-----LysThrTyr 31
Db 80 GCAGCTGATCTAGCAGACCTTTAAAGCAGAGATGACATGCACTTACCTGACGATCT 139
Qy 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
Db 140 ATTGACTTGACTAGCGATGACTGTGGCTCAACATACAGAGCTGTTACCAACCACTCC 199
Qy 52 AspThr-----GlnGlnGluAsnGlySerMetPheSerLeuIleThrTyrPheAsnIleAsp 69
Db 200 TCTACTGTGAACCAACAGAGATGAGACCATTTTACCTTTTACATGGAATATAGAT 259
Qy 70 GlyLeuAspLeuAenAenLeuSerGluArgAlaArgGlyValCysSerTyrlen 87
Db 260 GGCTTGATGATCAACAGCTTGACAGAGGGCTCGTGTATGTTCTGTGTTG 313

RESULT 194
LOCUS CR158280/c 744 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000371399412 Dog library Canis familiaris genomic,
GSS survey sequence.
ACCESSION CR158280
VERSION CR158280.1 GI:35285317
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 744)
Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.
Location/Qualifiers

FEATURES

source

1..744
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Alignment Scores:

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Score: 179.00 Matches: 34
Percent Similarity: 85.7% Conservative: 2

ORIGIN

Alignment Scores:

Pred. No.: 3,61e-12 Length: 831
Score: 179.00 Matches: 40
Percent Similarity: 62.2% Conservative: 21
Best Local Similarity: 40.8% Mismatches: 23
Query Match: 40.0% Indels: 14
DB: 6 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x CA981008 (1-831)

QY 3 ArgAlaLeuAenSerTyRPhgIuProProValGIuGluSerAlaLeuGIuArgPro 22
DB 25 AGGGGATCAATTCCTTGAAGCTGGGGG---GAGTCGACCTTACAAACAACT 81
QY 23 GluThr---IleSerGluPro-----LysThrTyr 31
DB 82 GCAGCTGATCTAGACACCTTTAAAGCAAGATGATGATGATGATGATGATGAT 141
QY 32 ValAspLeuThrAsnGluGluThrThraPserThrThraPserThraPserGlu 51
DB 142 ATTGACTGCTAGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 201
QY 52 AspThr-----GluGluGluAsnGlySerMetPheSerLeuIleThrThraPser 69
DB 202 TCTACTGTGAACCAACAAAGAAAGATGATGATGATGATGATGATGATGATGAT 261
QY 70 GlyLeuAspLeuAenAenSerGluArgAlaArgGlyValCysSerTyRleu 87
DB 262 GGCCTTGATGATCAACCGTTGACAGAGAGGCTCTGCTGATGATGATGATGAT 315

RESULT 197

CK797649 879 bp mRNA linear EST 25-FEB-2004
LOCUS AGENCOURT 18793748 NICHG XGC Te2N Xenopus laevis cDNA clone
DEFINITION IMAGE:720410 5', mRNA sequence.
ACCESSION CK797649
VERSION CK797649.1 GI:42809645
KEYWORDS EST.

SOURCE

Xenopus laevis (African clawed frog)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
BLDG 31 Rm10A07 Bethesda, MD 20892
Email: g9apbs-remail.nih.gov
Tissue Procurement: Igor B. David
cDNA Library Preparation: Express Genomics
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
http://image.llnl.gov
Plate: LHAM15083 row: m column: 16
High quality sequence stop: 730.
Location/Qualifiers

FEATURES

Source

1..879
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/lab_host="DH10B TONa"
/clone_id="NICHG XGC Te2N"
/note="Organ: testis; Vector: pExpress-1; Site:1. EcorV;
Location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.: 3,88e-12 Length: 879
Score: 179.00 Matches: 40
Percent Similarity: 62.2% Conservative: 21
Best Local Similarity: 40.8% Mismatches: 23
Query Match: 40.0% Indels: 14
DB: 7 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x CK797649 (1-879)

QY 3 ArgAlaLeuAenSerTyRPhgIuProProValGIuGluSerAlaLeuGIuArgPro 22
DB 12 AGGGGATCAATTCCTTGAAGCTGGGG---GAGTCGACCTTACAAACAACT 68
QY 23 GluThr---IleSerGluPro-----LysThrTyr 31
DB 69 GCAGCTGATCTAGACACCTTTAAAGCAAGATGATGATGATGATGATGATGAT 128
QY 32 ValAspLeuThrAsnGluGluThrThraPserThrThraPserThraPserGlu 51
DB 129 ATTGACTGCTAGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 188
QY 52 AspThr-----GluGluGluAsnGlySerMetPheSerLeuIleThrThraPser 69
DB 189 TCTACTGTGAACCAACAAAGAAAGATGATGATGATGATGATGATGATGATGAT 248
QY 70 GlyLeuAspLeuAenAenSerGluArgAlaArgGlyValCysSerTyRleu 87
DB 249 GGCCTTGATGATCAACCGTTGACAGAGAGGCTCTGCTGATGATGATGATGAT 302

RESULT 198

CA971409 896 bp mRNA linear EST 27-FEB-2003
LOCUS AGENCOURT 10764928 Wellcome CRC psk egg Xenopus laevis cDNA clone
DEFINITION IMAGE:6522803 5', mRNA sequence.
ACCESSION CA971409
VERSION CA971409.1 GI:27504063
KEYWORDS EST.

SOURCE

Xenopus laevis (African clawed frog)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: g9apbs-remail.nih.gov
Tissue Procurement: N. Garrett, P. Lemaire, A.M. Zorn, and J.B.
Gordon (Wellcome/CRC Institute)
cDNA Library Preparation: N. Garrett, P. Lemaire, A.M. Zorn, and
J.B. Gordon (Wellcome/CRC Institute)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XGC clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
http://image.llnl.gov
Plate: LHAM13764 row: p column: 04
High quality sequence stop: 611.
Location/Qualifiers

FEATURES

Source

Location/Qualifiers

J.B. Gurdon (Wellcome/CRC Institute)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L14M13773 row: e column: 22
High quality sequence stop: 698.
Location/Qualifiers

FEATURES
source

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/clone_lib="Wellcome CRC psk egg"
/note="Vector: pBluescript SK-; Site_1: NotI; Site_2:
EcoRI; cDNAs were oligo-dT primed and directionally
cloned. Library was constructed by N. Garrett, P. Lemaire,
A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute).
Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:

Pred. No.:	4,12e-12	Length:	919
Score:	179.00	Matches:	40
Percent Similarity:	62.2%	Conservative:	21
Best Local Similarity:	40.8%	Mismatches:	23
Query Match:	40.0%	Indels:	14
DB:	6	Gaps:	4

US-10-757-745-2_COPY_54_140 (1-87) x CA973696 (1-919)

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QY      3  ArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArgPro 22
          |||
Db      23  AGGGGATCATCTTCTTGGCTGGGGTG--GAGTGCACCTTACAAACAAACCT 79
          |||
QY      23  GluThr--IleSerGluPro-----LysThrTyr 31
          |||
Db      80  GCAGCTCATCTAGCAGACCTTTAAAGCAAGATGATGCAGTACCTCTGACCATGT 139
          |||
QY      32  ValAspLeuThrAnGluGluThrThrAspSerThrThrSerTyrIleSerProSerGlu 51
          |||
Db      140  ATTGACTGCTAGCTACGATGACTGTGGCTCAATCAGAAAGCTGTACACGAACTCC 199
          |||
QY      52  AspThr-----GlnGlnGluAenGlySerMetPheSerLeuIleThrTyrPaniIleAsp 69
          |||
Db      200  TCTACTGTGAACCAACAAAGATGAGCCCATTTTACCTTCTTACATGATATATAGAT 259
          |||
QY      70  G1yleuAepLeuAenAenLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
          |||
Db      260  GGCCTTGATGAATCAACGTTGCAGAGAGGCTCGTGTATATGTTCTGTGTTG 313
          |||
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Search completed: March 16, 2006, 04:56:59
Job time : 6904.46 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 16, 2006, 00:29:49 | Search time 549.738 Seconds
(without alignments)
595.756 Million cell updates/sec

Title: US-10-757-745-2_COPY_115_121

Perfect score: 38

Sequence: 1 SLITMNI 7

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 1000 summaries

Command line parameters:

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-O/abses/ABSSMB.spool/US10757745/runat_15032006_165652_3610/app.query.fasta_1
-DB=EST -QFMT=fasta -SUFFIX=rest -MINMATCH=0.1 -LOOPT=0 -LOOPT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biogum62 -TRANS=human40.cdi -LIST=1000
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=200 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEA=SITE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abses02h
-USER=US10757745 @CCN 1.8148 @runat_15032006_165652_3610 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LOGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	38	100.0	221	11	CR404572 Arabidops
3	38	100.0	227	11	CR094068 Forward s
4	38	100.0	246	10	CNS000VFS
5	38	100.0	289	1	BI125347 Arabidops
6	38	100.0	310	8	T26956 1d155proj
7	38	100.0	347	5	BU070378 im09c09.x

8	38	100.0	352	5	BQ787387 im09c09.y
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10	38	100.0	394	1	AV661333 AV661333
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13	38	100.0	463	8	DN651654 147331.B
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15	38	100.0	473	6	CB120234 K-EST0167
16	38	100.0	480	1	A1750554 CN04601.y
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18	38	100.0	511	5	B0659432 c147f06..z
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21	38	100.0	531	7	CN233559 KJ113F02
22	38	100.0	554	3	BP220985 BP220985
23	38	100.0	558	10	BK97515 Forward s
24	38	100.0	565	3	BP226620 BP226620
25	38	100.0	566	3	BP220508 BP220508
26	38	100.0	568	3	BP257211 BP257211
27	38	100.0	570	3	BM172060 imageqc_3
28	38	100.0	570	3	BP221518 BP221518
29	38	100.0	570	5	BU397611 603534313
30	38	100.0	572	3	BP262485 BP262485
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32	38	100.0	573	3	BP221260 BP221260
33	38	100.0	573	3	BP261500 BP261500
34	38	100.0	576	3	BP262642 BP262642
35	38	100.0	577	7	CN298919 170006001
36	38	100.0	580	3	BP261787 BP261787
37	38	100.0	580	3	BP274368 BP274368
38	38	100.0	581	1	AV1717253 AV1717253
39	38	100.0	581	3	BP199948 BP199948
40	38	100.0	581	3	BP207751 BP207751
41	38	100.0	581	3	BP225088 BP225088
42	38	100.0	581	3	BP262638 BP262638
43	38	100.0	581	3	BP264149 BP264149
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52	38	100.0	582	3	BP263516 BP263516
53	38	100.0	582	3	BP270415 BP270415
54	38	100.0	582	3	BP275810 BP275810
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57	38	100.0	583	3	BP262741 BP262741
58	38	100.0	583	3	BP319548 BP319548
59	38	100.0	583	5	BU783229 1n01a08..y
60	38	100.0	584	3	BP263059 BP263059
61	38	100.0	584	3	BP274942 BP274942
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63	38	100.0	588	3	BP236074 BP236074
64	38	100.0	588	3	BP348796 BP348796
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67	38	100.0	604	11	AV730762 AV730762
68	38	100.0	618	1	CR163431 Forward s
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71	38	100.0	634	6	CB157906 K-EST0217
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Thu Mar 16 10:39:26 2006

us-10-757-745-2 copy 115 121.rst

Page 2

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81	38	100.0	710	B164172	1172041.4	C 155	37	97.4	334	6	CB176715	AGNCCOURT
83	38	100.0	711	CN298923	170004008	C 156	37	97.4	404	6	BB116781	SCAP1927
84	38	100.0	720	CNS00X2P	AT089321	C 157	37	97.4	420	4	B2402954	CH230-399
85	38	100.0	729	CN298922	170004008	C 158	37	97.4	440	1	AA447219	HD4-911.8
85	38	100.0	739	CN298922	170004008	C 159	37	97.4	455	2	B8361212	HS-D-131A
86	38	100.0	731	CK160857	AGNCCOURT	C 160	37	97.4	455	2	B8361212	HS-D-131A
87	38	100.0	737	CK170843	AGNCCOURT	C 161	37	97.4	475	2	B8361212	HS-D-131A
88	38	100.0	739	CK170843	AGNCCOURT	C 162	37	97.4	504	1	B1459342	SCAP-3865
88	38	100.0	739	CK170843	AGNCCOURT	C 163	37	97.4	504	1	B1459342	SCAP-3865
89	38	100.0	751	CK170843	AGNCCOURT	C 164	37	97.4	504	1	B1459342	SCAP-3865
90	38	100.0	751	CK170843	AGNCCOURT	C 165	37	97.4	504	1	B1459342	SCAP-3865
91	38	100.0	752	CK170843	AGNCCOURT	C 166	37	97.4	504	1	B1459342	SCAP-3865
92	38	100.0	752	CK170843	AGNCCOURT	C 167	37	97.4	504	1	B1459342	SCAP-3865
93	38	100.0	752	CK170843	AGNCCOURT	C 168	37	97.4	504	1	B1459342	SCAP-3865
94	38	100.0	752	CK170843	AGNCCOURT	C 169	37	97.4	504	1	B1459342	SCAP-3865
95	38	100.0	752	CK170843	AGNCCOURT	C 170	37	97.4	504	1	B1459342	SCAP-3865
96	38	100.0	752	CK170843	AGNCCOURT	C 171	37	97.4	504	1	B1459342	SCAP-3865
97	38	100.0	752	CK170843	AGNCCOURT	C 172	37	97.4	504	1	B1459342	SCAP-3865
98	38	100.0	752	CK170843	AGNCCOURT	C 173	37	97.4	504	1	B1459342	SCAP-3865
99	38	100.0	752	CK170843	AGNCCOURT	C 174	37	97.4	504	1	B1459342	SCAP-3865
100	38	100.0	752	CK170843	AGNCCOURT	C 175	37	97.4	504	1	B1459342	SCAP-3865
101	38	100.0	752	CK170843	AGNCCOURT	C 176	37	97.4	504	1	B1459342	SCAP-3865
102	38	100.0	752	CK170843	AGNCCOURT	C 177	37	97.4	504	1	B1459342	SCAP-3865
103	38	100.0	752	CK170843	AGNCCOURT	C 178	37	97.4	504	1	B1459342	SCAP-3865
104	38	100.0	752	CK170843	AGNCCOURT	C 179	37	97.4	504	1	B1459342	SCAP-3865
105	38	100.0	752	CK170843	AGNCCOURT	C 180	37	97.4	504	1	B1459342	SCAP-3865
106	38	100.0	752	CK170843	AGNCCOURT	C 181	37	97.4	504	1	B1459342	SCAP-3865
107	38	100.0	752	CK170843	AGNCCOURT	C 182	37	97.4	504	1	B1459342	SCAP-3865
108	38	100.0	752	CK170843	AGNCCOURT	C 183	37	97.4	504	1	B1459342	SCAP-3865
109	38	100.0	752	CK170843	AGNCCOURT	C 184	37	97.4	504	1	B1459342	SCAP-3865
110	38	100.0	752	CK170843	AGNCCOURT	C 185	37	97.4	504	1	B1459342	SCAP-3865
111	38	100.0	752	CK170843	AGNCCOURT	C 186	37	97.4	504	1	B1459342	SCAP-3865
112	38	100.0	752	CK170843	AGNCCOURT	C 187	37					

227	C	228	36	94.7	340	10	CNS00VYT	AT092915 Arabidops	C	300	36	94.7	650	8	CX682689	CX682689 ydf1h03.
228	C	229	36	94.7	365	10	CZ013997	CZ013997 CH240_509	C	301	36	94.7	651	1	AV764049	AV764049 AV764049
229	C	230	36	94.7	397	7	CV417002	CV417002 RC3-HT023	C	302	36	94.7	651	1	AM186402	AM186402 zef1c12.y
230	C	231	36	94.7	405	7	CK100804	CK100804 C089P96.5	C	303	36	94.7	657	7	CV008065	CV008065 zef101-14M
231	C	232	36	94.7	408	2	BE450436	BE450436 EST401323	C	304	36	94.7	658	7	CO688138	CO688138 DG11-241e
232	C	233	36	94.7	415	1	AV648795	AV648795 AV648795	C	305	36	94.7	661	8	DN123584	DN123584 1123895.M
233	C	234	36	94.7	422	1	AA774547	AA774547 a127a12.8	C	306	36	94.7	663	5	BM040519	BM040519 BM040519
234	C	235	36	94.7	432	9	BZ414332	BZ414332 lf24a08.y	C	307	36	94.7	664	7	DN123917	DN123917 1124279.M
235	C	236	36	94.7	440	6	CD676972	CD676972 ho09c11.y	C	308	36	94.7	666	7	CO050979	CO050979 le.m0.21
236	C	237	36	94.7	441	1	BU122526	BU122526 BU122526	C	309	36	94.7	671	2	BB644882	BB644882 BB644882
237	C	238	36	94.7	446	1	AI539304	AI539304 tes0h09.x	C	310	36	94.7	678	2	BG542014	BG542014 602572126
238	C	239	36	94.7	455	5	AQ245357	AQ245357 HS_2062.A	C	311	36	94.7	679	7	CK761472	CK761472 atp02-7ms
239	C	240	36	94.7	467	5	BX103806	BX103806 BX103806	C	312	36	94.7	680	3	BP439654	BP439654 BP439654
240	C	241	36	94.7	476	2	BR554376	BR554376 EST355719	C	313	36	94.7	681	10	CW384830	CW384830 fdbb001f0
241	C	242	36	94.7	477	1	AA850361	AA850361 EST193128	C	314	36	94.7	692	2	BB339396	BB339396 BB339396
242	C	243	36	94.7	482	1	AU084430	AU084430 AU084430	C	315	36	94.7	692	5	BM317951	BM317951 BM317951
243	C	244	36	94.7	482	1	AU243350	AU243350 AU243350	C	316	36	94.7	693	3	BM317951	BM317951 EST515244
244	C	245	36	94.7	483	1	BM759885	BM759885 K-EST0040	C	317	36	94.7	694	2	BG889393	BG889393 EST515244
245	C	246	36	94.7	486	9	AZ927442	AZ927442 476.d1875	C	318	36	94.7	694	5	BM329060	BM329060 BM329060
246	C	247	36	94.7	488	1	AU084166	AU084166 AU084166	C	319	36	94.7	694	7	CV689182	CV689182 sjf4-010
247	C	248	36	94.7	488	10	CL326524	CL326524 RPT44_24	C	320	36	94.7	694	7	DN090145	DN090145 57918.2.D
248	C	249	36	94.7	491	3	BP174136	BP174136 BP174136	C	321	36	94.7	695	5	BM050262	BM050262 BM050262
249	C	250	36	94.7	493	1	AI913404	AI913404 wallh01.x	C	322	36	94.7	697	10	AG083539	AG083539 Pan.trog1
250	C	251	36	94.7	504	5	BM687258	BM687258 BM687258	C	323	36	94.7	701	9	AZ836944	AZ836944 2M0132H01
251	C	252	36	94.7	506	1	AU085609	AU085609 AU085609	C	324	36	94.7	701	9	AG380783	AG380783 Mus.muscu
252	C	253	36	94.7	506	5	BU429399	BU429399 UT-HF-BNO	C	325	36	94.7	712	2	BG600004	BG600004 EST504899
253	C	254	36	94.7	517	2	BG490289	BG490289 602519276	C	326	36	94.7	712	10	AG380783	AG380783 Mus.muscu
254	C	255	36	94.7	519	5	BY478479	BY478479 BY478479	C	327	36	94.7	718	10	AG370600	AG370600 Mus.muscu
255	C	256	36	94.7	528	1	AM082245	AM082245 xb64d08.x	C	328	36	94.7	721	5	BU349289	BU349289 604170832
256	C	257	36	94.7	530	1	AU085589	AU085589 AU085589	C	329	36	94.7	721	5	BU349289	BU349289 604170832
257	C	258	36	94.7	533	1	AQ080634	AQ080634 HS_5444.A	C	330	36	94.7	725	5	BU620793	BU620793 UT-H-FUL-
258	C	259	36	94.7	536	2	BT183317	BT183317 602934494	C	331	36	94.7	726	2	BG888791	BG888791 EST511462
259	C	260	36	94.7	539	7	CK418493	CK418493 AUF-Ipova	C	332	36	94.7	733	3	BX433112	BX433112 BX433112
260	C	261	36	94.7	541	10	CE738056	CE738056 t1gr-988-	C	333	36	94.7	734	10	AG370646	AG370646 ZMMBRC034
261	C	262	36	94.7	541	1	AA850362	AA850362 EST193129	C	334	36	94.7	734	10	AG370646	AG370646 ZMMBRC034
262	C	263	36	94.7	548	5	BZ441860	BZ441860 BOMK41TR	C	335	36	94.7	735	10	AG370646	AG370646 ZMMBRC034
263	C	264	36	94.7	548	5	BK498549	BK498549 DKFZP779C	C	336	36	94.7	735	10	AG370646	AG370646 ZMMBRC034
264	C	265	36	94.7	549	1	AI102752	AI102752 EST712041	C	337	36	94.7	735	10	AG370646	AG370646 ZMMBRC034
265	C	266	36	94.7	551	10	CW769390	CW769390 OG-BM8008	C	338	36	94.7	735	10	AG370646	AG370646 ZMMBRC034
266	C	267	36	94.7	554	2	BE831012	BE831012 PM3-MT003	C	339	36	94.7	740	6	CB241751	CB241751 UT-CF-BNO
267	C	268	36	94.7	555	3	BP273441	BP273441 BP273441	C	340	36	94.7	740	9	BH670089	BH670089 BOMHP5TR
268	C	269	36	94.7	555	3	BP243301	BP243301 BP243301	C	341	36	94.7	750	9	CE114365	CE114365 t1gr-988-
269	C	270	36	94.7	557	2	BF432058	BF432058 nab85b05.	C	342	36	94.7	752	10	DU013249	DU013249 290631.T0
270	C	271	36	94.7	560	7	CF979138	CF979138 2-84-RP2.	C	343	36	94.7	755	5	BU330556	BU330556 603871430
271	C	272	36	94.7	561	9	CC971634	CC971634 ZUDN31TV	C	344	36	94.7	758	9	CC311835	CC311835 TAM32-21L
272	C	273	36	94.7	566	5	CC630759	CC630759 DG9-54m16	C	345	36	94.7	760	10	BZ982967	BZ982967 PUCB148TD
273	C	274	36	94.7	572	5	EX101254	EX101254 BX101254	C	346	36	94.7	765	9	BX179463	BX179463 Danilo.rer
274	C	275	36	94.7	572	6	CD874493	CD874493 AZ03.102E	C	347	36	94.7	772	7	BN080859	BN080859 11c05f08.
275	C	276	36	94.7	572	9	AZ610019	AZ610019 1M0435N05	C	348	36	94.7	773	10	CG308284	CG308284 OAZBR41TH
276	C	277	36	94.7	576	10	CZ488472	CZ488472 f05847-3P	C	349	36	94.7	777	11	CR957777	CR957777 Homo.sapl
277	C	278	36	94.7	576	7	CK978333	CK978333 4109792.B	C	350	36	94.7	783	2	BF460250	BF460250 073C11.Ma
278	C	279	36	94.7	578	9	BI6785	BI6785 343G24.TVB	C	351	36	94.7	794	5	BU443384	BU443384 604143791
279	C	280	36	94.7	581	10	CZ844186	CZ844186 OC_Ba023	C	352	36	94.7	800	7	CV488192	CV488192 AGENCOURT
280	C	281	36	94.7	582	9	CK425830	CK425830 AUF_IPTes	C	353	36	94.7	802	9	CC499669	CC499669 CH240.337
281	C	282	36	94.7	584	2	CE098038	CE098038 t1gr-988-	C	354	36	94.7	807	2	BF688990	BF688990 60218E234
282	C	283	36	94.7	588	2	BG029072	BG029072 602292537	C	355	36	94.7	820	7	CR773025	CR773025 DKFZP470F
283	C	284	36	94.7	588	2	BG543305	BG543305 602573636	C	356	36	94.7	822	7	CV506257	CV506257 72936.1.M
284	C	285	36	94.7	588	2	AQ048890	AQ048890 CLM-1091-	C	357	36	94.7	828	7	CV477960	CV477960 57918.1.D
285	C	286	36	94.7	592	9	BH312895	BH312895 CH230-168	C	358	36	94.7	830	11	BP447602	BP447602 BP447602
286	C	287	36	94.7	596	9	BZ672796	BZ672796 PUBDW85TD	C	359	36	94.7	831	10	CR330444	CR330444 ZMMBRC037
287	C	288	36	94.7	599	10	AG924737	AG924737 PROS0H11	C	360	36	94.7	832	1	AU085662	AU085662 AU085662
288	C	289	36	94.7	603	5	BM514814	BM514814 kyo8h01.y	C	361	36	94.7	832	7	CO077683	CO077683 GR_Ba39J
289	C	290	36	94.7	605	3	BM514814	BM514814 kyo8h01.y	C	362	36	94.7	835	10	DU021996	DU021996 1726.Toma
290	C	291	36	94.7	606	7	CV688321	CV688321 sjf4-012-	C	363	36	94.7	847	9	CC912629	CC912629 f072h04ba
291	C	292	36	94.7	606	7	CV688321	CV688321 sjf4-012-	C	364	36	94.7	847	10	CG000036	CG000036 ZUAGV68TH
292	C	293	36	94.7	615	3	BM514326	BM514326 kx99h11.y	C	365	36	94.7	849	11	CR059365	CR059365 Forward.s
293	C	294	36	94.7	616	2	BG098893	BG098893 EST463424	C	366	36	94.7	851	5	BU122825	BU122825 603147289
294	C	295	36	94.7	616	10	CM460655	CM460655 fdbb001f2	C	367	36	94.7	853	10	BM360760	BM360760 Forward.s
295	C	296	36	94.7	619	8	DR000172	DR000172 TCI03151	C	368	36	94.7	853	10	CR213969	CR213969 Forward.s
296	C	297	36	94.7	620	10	CZ770509	CZ770509 OC_Ba012	C	369	36	94.7	854	11	DU003230	DU003230 285791.T0
297	C	298	36	94.7	624	6	CF262707	CF262707 AUA_Ipova	C	370	36	94.7	855	3	BP447680	BP447680 BP447680
298	C	299	36	94.7	631	3	BM820383	BM820383 K-EST0088	C	371	36	94.7	862	10	CG769607	CG769607 TCB51.1.G
299	C	300	36	94.7	636	2	BE822210	BE822210 GM700016B	C	372	36	94.7	862	10	CG769607	CG769607 TCB51.1.G

C 519	35	92.1	590	10	CE779884	CE779884	tigr-g88-	C 592	35	92.1	753	6	CD613378	CD613378	56044145H
C 520	35	92.1	591	7	CN429952	CN429952	170006000	C 593	35	92.1	761	10	CG672819	CG672819	tr80551 t
C 521	35	92.1	591	9	AO195155	AO195155	RPC111-61	C 594	35	92.1	763	9	A2720213	A2720213	RPCI-24-1
C 522	35	92.1	593	11	CR074393	CR074393	Reverse b	C 595	35	92.1	765	7	CN042095	CN042095	v11_p41 a
C 523	35	92.1	595	1	A1786794	A1786794	u157h08.x	C 596	35	92.1	771	11	CR030301	CR030301	Sus scrofa
C 524	35	92.1	595	3	B1839807	B1839807	fc43604.y	C 597	35	92.1	777	10	AG544964	AG544964	Sus scrofa
C 525	35	92.1	596	7	CO842378	CO842378	LM_GLS_00	C 598	35	92.1	779	3	BP447155	BP447155	BP447155
C 526	35	92.1	602	11	CR022286	CR022286	tigr-g88- b	C 599	35	92.1	779	10	CG5858102	CG5858102	ZMMB6026
C 527	35	92.1	608	11	CR253488	CR253488	Reverse b	C 600	35	92.1	780	5	BM407552	BM407552	BM407552
C 528	35	92.1	610	9	AQ378909	AQ378909	RPC111-16	C 601	35	92.1	781	9	BM711050	BM711050	BM711050
C 529	35	92.1	615	2	BF446814	BF446814	7G92604.x	C 602	35	92.1	791	3	B1818156	B1818156	60303239F
C 530	35	92.1	616	4	CNS0A79H	CNS0A79H	Arabiadops	C 603	35	92.1	794	5	BK433384	BK433384	BK433384
C 531	35	92.1	620	10	CM869280	CM869280	sh52kd15-	C 604	35	92.1	798	5	BK658761	BK658761	BK658761
C 532	35	92.1	622	1	AV988429	AV988429	AY988429	C 605	35	92.1	798	10	CG222221	CG222221	CG222221
C 533	35	92.1	623	7	CR791374	CR791374	DKP2p468F	C 606	35	92.1	802	7	CR374764	CR374764	CR374764
C 534	35	92.1	623	10	CE284103	CE284103	tigr-g88-	C 607	35	92.1	802	10	DU032104	DU032104	13515 Tom
C 535	35	92.1	626	2	BF977971	BF977971	602148451	C 608	35	92.1	807	10	C2140753	C2140753	BF572737
C 536	35	92.1	630	6	CA377612	CA377612	656226 NC	C 609	35	92.1	811	2	BF572737	BF572737	BF572737
C 537	35	92.1	634	10	CE454443	CE454443	tigr-g88-	C 610	35	92.1	811	7	CVA85714	CVA85714	CVA85714
C 538	35	92.1	636	10	CM271605	CM271605	104_743.1	C 611	35	92.1	812	7	CO484948	CO484948	CO484948
C 539	35	92.1	639	6	CB128927	CB128927	K-EST0178	C 612	35	92.1	815	1	AU119201	AU119201	AU119201
C 540	35	92.1	640	2	BG530594	BG530594	602560183	C 613	35	92.1	822	10	AG827693	AG827693	AG827693
C 541	35	92.1	641	10	AG039320	AG039320	Pan trogl	C 614	35	92.1	826	6	CB198199	CB198199	CB198199
C 542	35	92.1	641	10	CE316686	CE316686	tigr-g88-	C 615	35	92.1	826	7	CR991326	CR991326	CR991326
C 543	35	92.1	642	1	AV352778	AV352778	AV352778	C 616	35	92.1	826	9	BH531176	BH531176	BH531176
C 544	35	92.1	643	6	CB504779	CB504779	bsa1p1b5	C 617	35	92.1	836	8	DR556593	DR556593	DR556593
C 545	35	92.1	643	6	CF791206	CF791206	879373 MA	C 618	35	92.1	840	5	B1910605	B1910605	603069820
C 546	35	92.1	645	10	CL545729	CL545729	OB_Ba007	C 619	35	92.1	845	3	CC473467	CC473467	CC473467
C 547	35	92.1	646	8	DR682551	DR682551	EST107262	C 620	35	92.1	845	10	CG127395	CG127395	CG127395
C 548	35	92.1	646	9	AO208336	AO208336	HS_3233_A	C 621	35	92.1	855	9	BQ225937	BQ225937	BQ225937
C 549	35	92.1	648	2	BG749828	BG749828	602708215	C 622	35	92.1	859	3	BF125724	BF125724	BF125724
C 550	35	92.1	648	10	CM328125	CM328125	104_824.1	C 623	35	92.1	871	2	CN316340	CN316340	CN316340
C 551	35	92.1	649	3	B1428503	B1428503	1484h06.y	C 624	35	92.1	873	7	BK367118	BK367118	BK367118
C 552	35	92.1	652	6	CD613374	CD613374	56016113H	C 625	35	92.1	874	5	AL525084	AL525084	AL525084
C 553	35	92.1	652	6	CD697941	CD697941	EST16265	C 626	35	92.1	876	1	AL525084	AL525084	AL525084
C 554	35	92.1	661	6	CD613377	CD613377	56016205J	C 627	35	92.1	883	10	CG2427883	CG2427883	CG2427883
C 555	35	92.1	665	9	BZ902708	BZ902708	CH240_23G	C 628	35	92.1	888	2	BG760728	BG760728	BG760728
C 556	35	92.1	669	10	CL345730	CL345730	RPCI44_28	C 629	35	92.1	888	8	DR564952	DR564952	DR564952
C 557	35	92.1	671	2	BG257494	BG257494	602377635	C 630	35	92.1	891	10	CG2229235	CG2229235	CG2229235
C 558	35	92.1	675	10	CZ413367	CZ413367	1009670 R	C 631	35	92.1	891	11	CR247314	CR247314	CR247314
C 559	35	92.1	681	10	CM422980	CM422980	FBBD0111	C 632	35	92.1	892	2	BG681544	BG681544	BG681544
C 560	35	92.1	682	10	CM28124	CM28124	104_824.1	C 633	35	92.1	894	5	BQ959150	BQ959150	BQ959150
C 561	35	92.1	683	7	CM429957	CM429957	170004240	C 634	35	92.1	895	2	BG284589	BG284589	BG284589
C 562	35	92.1	684	1	AM271333	AM271333	x446e12.x	C 635	35	92.1	896	7	CG222300	CG222300	CG222300
C 563	35	92.1	684	6	CF123056	CF123056	UI-HF-C80	C 636	35	92.1	902	1	AL521869	AL521869	AL521869
C 564	35	92.1	686	11	CR225097	CR225097	Reverse b	C 637	35	92.1	904	4	AL558885	AL558885	AL558885
C 565	35	92.1	686	11	CR220024	CR220024	Sus scrofa	C 638	35	92.1	904	10	CG127398	CG127398	CG127398
C 566	35	92.1	687	10	CL176646	CL176646	104_383.1	C 639	35	92.1	906	5	BQ421907	BQ421907	BQ421907
C 567	35	92.1	688	5	BX118132	BX118132	Reverse b	C 640	35	92.1	907	7	CO214584	CO214584	CO214584
C 568	35	92.1	689	5	BX101161	BX101161	Reverse b	C 641	35	92.1	909	5	BK350887	BK350887	BK350887
C 569	35	92.1	690	8	CK032449	CK032449	1344691 N	C 642	35	92.1	914	8	DN569815	DN569815	DN569815
C 570	35	92.1	691	5	BM314431	BM314431	Reverse b	C 643	35	92.1	924	4	CNS013YU	CNS013YU	CNS013YU
C 571	35	92.1	691	10	CE427525	CE427525	tigr-g88-	C 644	35	92.1	929	5	BU188090	BU188090	BU188090
C 572	35	92.1	699	2	BE327599	BE327599	lv78c10.x	C 645	35	92.1	932	8	DR469360	DR469360	DR469360
C 573	35	92.1	700	6	CD613379	CD613379	56046145J	C 646	35	92.1	936	10	DU064014	DU064014	DU064014
C 574	35	92.1	700	7	DN271400	DN271400	LRB30321	C 647	35	92.1	940	5	BU501460	BU501460	BU501460
C 575	35	92.1	701	7	CN289884	CN289884	170005999	C 648	35	92.1	940	5	BK371705	BK371705	BK371705
C 576	35	92.1	702	10	CE750616	CE750616	tigr-g88-	C 649	35	92.1	941	5	BU165600	BU165600	BU165600
C 577	35	92.1	704	7	CK469489	CK469489	Reverse b	C 650	35	92.1	943	3	B1838538	B1838538	B1838538
C 578	35	92.1	706	7	CO682628	CO682628	DLG11-156n	C 651	35	92.1	943	3	B0066929	B0066929	B0066929
C 579	35	92.1	706	10	CE572671	CE572671	tigr-g88-	C 652	35	92.1	953	3	B1412669	B1412669	B1412669
C 580	35	92.1	708	7	CM429954	CM429954	170006002	C 653	35	92.1	963	7	CV662530	CV662530	CV662530
C 581	35	92.1	712	10	CG254919	CG254919	OC4B808TC	C 654	35	92.1	993	2	BG171102	BG171102	BG171102
C 582	35	92.1	714	9	AQ888368	AQ888368	HS_4811_A	C 655	35	92.1	1003	10	CG290972	CG290972	CG290972
C 583	35	92.1	716	9	CC371343	CC371343	PUEFH2TD	C 656	35	92.1	1005	2	BG433325	BG433325	BG433325
C 584	35	92.1	719	9	CC434348	CC434348	PUEFH2TD	C 657	35	92.1	1014	1	AL532711	AL532711	AL532711
C 585	35	92.1	723	7	CO731498	CO731498	Mus muscu	C 658	35	92.1	1055	1	BU444079	BU444079	BU444079
C 586	35	92.1	724	10	AG290105	AG290105	Mus muscu	C 659	35	92.1	1075	5	BM242364	BM242364	BM242364
C 587	35	92.1	736	6	CD613373	CD613373	56016105J	C 660	35	92.1	1076	3	BM23374	BM23374	BM23374
C 588	35	92.1	739	6	CD357236	CD357236	AGENCOURT	C 661	35	92.1	1079	3	BE732095	BE732095	BE732095
C 589	35	92.1	742	6	CD357236	CD357236	AGENCOURT	C 662	35	92.1	1080	2	BM907926	BM907926	BM907926
C 590	35	92.1	744	10	CG674206	CG674206	104_635.1	C 663	35	92.1	1101	10	CNS0153H	CNS0153H	CNS0153H
C 591	35	92.1	750	10	CG674206	CG674206	tr81938 t	C 664	35	92.1	1110	3	BM907926	BM907926	BM907926

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665	35	92.1	1150	3	BMS47543	BMS47543	AGENCOURT	C 738	34	89.5	274	1	A1672240	A1672240
666	35	92.1	1132	7	CRS52001	CRS52001	CRS52001	C 739	34	89.5	274	2	BPS26104	BPS26104
667	35	92.1	1657	4	CNS0A637	BX622153	ArabiIdop8	C 740	34	89.5	274	2	BE182968	BE182968
668	35	92.1	1768	4	CRS96540	CRS96540	full1-1eng	C 741	34	89.5	274	2	BE183019	BE183019
669	35	92.1	1812	4	CR604027	CR604027	full1-1eng	C 742	34	89.5	275	1	AM496819	AM496819
670	35	92.1	2019	8	CR858411	CR858411	Pong6 PY3	C 743	34	89.5	276	2	BP339845	BP339845
671	34	89.5	69	8	H87983	H87983	Y18B06.t1	C 744	34	89.5	276	2	AA483945	AA483945
672	34	89.5	71	1	AA758458	AA758458	z117604.8	C 745	34	89.5	279	1	AA291592	AA291592
673	34	89.5	94	1	AA553989	AA553989	nk35406.8	C 746	34	89.5	280	1	AA287332	AA287332
674	34	89.5	105	1	AA604975	AA604975	no93407.8	C 747	34	89.5	288	6	BM454494	BM454494
675	34	89.5	106	9	BH343509	BH343509	CH230-195	C 748	34	89.5	289	6	CA228526	CA228526
676	34	89.5	113	1	A1745029	A1745029	tr18B07.X	C 749	34	89.5	290	5	BM462336	BM462336
677	34	89.5	119	8	DR115000	DR115000	1432735 M	C 750	34	89.5	291	9	AO098899	AO098899
678	34	89.5	119	10	CM132573	CM132573	104.516.1	C 751	34	89.5	292	1	A1558445	A1558445
679	34	89.5	119	10	AL767139	AL767139	ArabiIdop8	C 752	34	89.5	292	9	B14491	B14491
680	34	89.5	121	2	BE241526	BE241526	TCAP1D07	C 753	34	89.5	294	1	A1780778	A1780778
681	34	89.5	121	7	CR972770	CR972770	4103340 B	C 754	34	89.5	295	2	BP346677	BP346677
682	34	89.5	147	1	AV773145	AV773145	AV773145	C 755	34	89.5	297	2	BM448908	BM448908
683	34	89.5	148	7	CK013947	CK013947	25351.rstC	C 756	34	89.5	298	10	CC468288	CC468288
684	34	89.5	155	1	BB084026	BB084026	BB084026	C 757	34	89.5	300	2	BM170082	BM170082
685	34	89.5	155	10	CM054029	CM054029	104.294.1	C 758	34	89.5	301	1	AA349844	AA349844
686	34	89.5	159	2	BE182967	BE182967	CM2-HT06.5	C 759	34	89.5	301	9	CC156978	CC156978
687	34	89.5	159	2	BE183022	BE183022	CM4-HT06.5	C 760	34	89.5	301	9	CC156978	CC156978
688	34	89.5	159	3	BM151270	BM151270	TCBAP1D47	C 761	34	89.5	302	3	BT132355	BT132355
689	34	89.5	164	1	AM000364	AM000364	614014C04	C 762	34	89.5	303	9	CC176310	CC176310
690	34	89.5	164	2	BC993153	BC993153	RC4-HT125	C 763	34	89.5	304	1	AA659356	AA659356
691	34	89.5	165	2	BG004517	BG004517	TI10-GN028	C 764	34	89.5	304	1	BP175607	BP175607
692	34	89.5	169	8	DI9798	DI9798	HUMGS00754	C 765	34	89.5	304	6	DM253237	DM253237
693	34	89.5	170	2	BF801486	BF801486	RC0-CI006	C 766	34	89.5	305	1	A1932579	A1932579
694	34	89.5	171	2	BF801480	BF801480	RC0-CI006	C 767	34	89.5	309	6	BP338158	BP338158
695	34	89.5	178	6	CP971056	CP971056	OAD2C09.8	C 768	34	89.5	309	6	AO488748	AO488748
696	34	89.5	180	10	CG549568	CG549568	OST153191	C 769	34	89.5	310	5	BM081673	BM081673
697	34	89.5	183	1	AU071401	AU071401	AU071401	C 770	34	89.5	310	5	CP640300	CP640300
698	34	89.5	184	5	BM261170	BM261170	BM261170	C 771	34	89.5	310	7	CN293426	CN293426
699	34	89.5	193	1	AU071400	AU071400	AU071400	C 772	34	89.5	318	1	A1282358	A1282358
700	34	89.5	196	1	A1558931	A1558931	EP78B04.Y	C 773	34	89.5	318	6	BM114252	BM114252
701	34	89.5	201	1	AA358492	AA358492	EST67371	C 774	34	89.5	319	10	CG687436	CG687436
702	34	89.5	201	2	BE954308	BE954308	UR-M-CE1-	C 775	34	89.5	321	9	CC970889	CC970889
703	34	89.5	204	7	CN228381	CN228381	RJB039808	C 776	34	89.5	321	9	AO071778	AO071778
704	34	89.5	205	9	AQ110419	AQ110419	CTT-HSP-2	C 777	34	89.5	321	2	BM422395	BM422395
705	34	89.5	208	2	BI040769	BI040769	CM3-WT026	C 778	34	89.5	321	6	AA140354	AA140354
706	34	89.5	209	1	AW773579	AW773579	EST332399	C 779	34	89.5	322	6	AA140354	AA140354
707	34	89.5	210	1	AA368707	AA368707	EST80003	C 780	34	89.5	323	1	AU177932	AU177932
708	34	89.5	212	11	CR398155	CR398155	ArabiIdop8	C 781	34	89.5	323	5	BM277970	BM277970
709	34	89.5	213	11	TA15H08P	TA15H08P	ArabiIdop8	C 782	34	89.5	323	5	BM277970	BM277970
710	34	89.5	224	1	BB068713	BB068713	BB068713	C 783	34	89.5	323	2	BM508026	BM508026
711	34	89.5	226	2	BB248749	BB248749	BB248749	C 784	34	89.5	325	3	BM168742	BM168742
712	34	89.5	227	3	BQ316249	BQ316249	MR1-CT005	C 785	34	89.5	325	3	A1368333	A1368333
713	34	89.5	230	1	BB148743	BB148743	BB148743	C 786	34	89.5	327	1	A1368333	A1368333
714	34	89.5	230	2	BG230454	BG230454	nr146f05.	C 787	34	89.5	340	1	A1218313	A1218313
715	34	89.5	235	1	BB061587	BB061587	BB061587	C 788	34	89.5	342	9	BZ236163	BZ236163
716	34	89.5	239	1	AV244207	AV244207	AV244207	C 789	34	89.5	343	8	CY332100	CY332100
717	34	89.5	240	8	DT054060	DT054060	COT.FY.CO	C 790	34	89.5	343	8	W0321	W0321
718	34	89.5	240	9	AZ835688	AZ835688	2M0T10M07	C 791	34	89.5	343	11	CK079005	CK079005
719	34	89.5	243	2	BB418668	BB418668	BB418668	C 792	34	89.5	343	11	AA253687	AA253687
720	34	89.5	244	2	AA284514	AA284514	rr20C08.8	C 793	34	89.5	346	8	F11140	F11140
721	34	89.5	244	2	BB510881	BB510881	BB510881	C 794	34	89.5	346	8	A1494121	A1494121
722	34	89.5	245	1	AA293269	AA293269	rr33B08.8	C 795	34	89.5	346	8	A1494121	A1494121
723	34	89.5	246	1	AA478990	AA478990	rr33B08.8	C 796	34	89.5	346	8	A1494121	A1494121
724	34	89.5	247	2	BF083169	BF083169	OV0-CS001	C 797	34	89.5	346	8	A1494121	A1494121
725	34	89.5	250	1	A1829601	A1829601	w22Bh02.X	C 798	34	89.5	346	8	A1494121	A1494121
726	34	89.5	253	2	BF365339	BF365339	OV3-WT002	C 799	34	89.5	353	2	CC688126	CC688126
727	34	89.5	255	6	CD543921	CD543921	BO253C07-	C 800	34	89.5	354	6	AA699256	AA699256
728	34	89.5	257	2	BE540175	BE540175	EST820331	C 801	34	89.5	356	3	AA699256	AA699256
729	34	89.5	257	7	BE540175	BE540175	601062025	C 802	34	89.5	358	3	BM464412	BM464412
730	34	89.5	258	1	AA573076	AA573076	rm50603.8	C 803	34	89.5	360	8	BB805805	BB805805
731	34	89.5	261	1	AU156333	AU156333	AU156333	C 804	34	89.5	360	10	DM844103	DM844103
732	34	89.5	261	3	BB874809	BB874809	BB874809	C 805	34	89.5	362	1	AA686804	AA686804
733	34	89.5	268	3	AA700774	AA700774	2166411.8	C 806	34	89.5	362	1	AA686804	AA686804
734	34	89.5	269	1	A1022390	A1022390	cw72E05.X	C 807	34	89.5	362	1	AA686804	AA686804
735	34	89.5	272	1	AA974011	AA974011	CQ12510.8	C 808	34	89.5	364	2	BB587334	BB587334
736	34	89.5	273	1	AV150081	AV150081	AV150081	C 809	34	89.5	365	1	AA634166	AA634166
737	34	89.5	273	1	AV150081	AV150081	AV150081	C 810	34	89.5	366	1	AA634166	AA634166

811	34	89.5	367	1	AI500190	AI500190	cm93g03.x	884	34	89.5	413	1	AA716177	AA716177	zg63g09.s
812	34	89.5	367	5	BK485809	BK485809	DKF2656K	885	34	89.5	413	3	BP663093	BP663093	BP663093
813	34	89.5	369	1	AM105542	AM105542	xd54507.x	886	34	89.5	413	6	CA634743	CA634743	w1e1n.pk0
814	34	89.5	369	1	AM150665	AM150665	xf64b12.x	887	34	89.5	413	9	B2240464	B2240464	ch230-362
815	34	89.5	370	8	BI710424	BI710424	fg36c08.x	888	34	89.5	414	1	AI198843	AI198843	qf54g12.x
816	34	89.5	370	8	W95326	W95326	ze01a10.s	889	34	89.5	414	1	AM510448	AM510448	hbl5g04.x
817	34	89.5	371	2	BF313182	BF313182	601896514	890	34	89.5	414	3	BM151177	BM151177	TCBAP1D13
818	34	89.5	371	2	BF316870	BF316870	601903389	891	34	89.5	414	3	BQ346405	BQ346405	PM4-WT003
819	34	89.5	371	9	AQ095269	AQ095269	HS-3027.A	892	34	89.5	416	1	AI721083	AI721083	aa69h02.x
820	34	89.5	372	9	BY423458	BY423458	BY423458	893	34	89.5	416	2	BB693667	BB693667	BB693667
821	34	89.5	372	9	BZ660463	BZ660463	SALK_0239	894	34	89.5	417	3	BJ788572	BJ788572	BJ788572
822	34	89.5	373	1	AL843589	AL843589	AL843589	895	34	89.5	417	3	BM151491	BM151491	TCBAP1D92
823	34	89.5	373	1	BM464938	BM464938	AGENCOURT	896	34	89.5	417	8	R32810	R32810	yh71b01.s
824	34	89.5	374	1	AA053181	AA053181	2173h07.s	897	34	89.5	417	9	A2144351	A2144351	SP-0020.B
825	34	89.5	375	1	AI239471	AI239471	qm95h04.x	898	34	89.5	417	10	CG495985	CG495985	OST35740
826	34	89.5	375	1	AV939968	AV939968	AV939968	899	34	89.5	419	1	AA057297	AA057297	zk70F06.x
827	34	89.5	375	2	BE242446	BE242446	TCAP1D14	900	34	89.5	419	10	CM687277	CM687277	OG-BBA004
828	34	89.5	376	3	BM356966	BM356966	161-CA.Tr	901	34	89.5	420	1	AJ470572	AJ470572	AJ470572
829	34	89.5	377	2	BI262918	BI262918	NP026C06P	902	34	89.5	420	3	BM687934	BM687934	UI-E-CX1-
830	34	89.5	379	1	AM002270	AM002270	WC84503.x	903	34	89.5	421	7	CO151209	CO151209	EST826282
831	34	89.5	379	1	AA358004	AA358004	EST66852	904	34	89.5	422	10	CL824386	CL824386	OR-CBA004
832	34	89.5	380	1	AI075067	AI075067	cu61h03.x	905	34	89.5	422	1	AV951401	AV951401	AV951401
833	34	89.5	381	1	AL843647	AL843647	AL843647	906	34	89.5	423	1	CX781899	CX781899	HESC3_10-
834	34	89.5	381	1	AUI49633	AUI49633	AUI49633	907	34	89.5	423	8	AV951401	AV951401	AV951401
835	34	89.5	382	1	AA362651	AA362651	EST72373	908	34	89.5	424	1	AUI59216	AUI59216	AUI59216
836	34	89.5	382	1	AA582813	AA582813	nm35d12.s	909	34	89.5	424	2	BF088912	BF088912	PM3-HT050
837	34	89.5	382	8	DR171224	DR171224	26-E07.A	910	34	89.5	424	3	BQ029089	BQ029089	UI-H-DT0-
838	34	89.5	383	1	AL843231	AL843231	AL843231	911	34	89.5	424	9	CE253367	CE253367	UI-CF-FNO
839	34	89.5	384	2	BF609050	BF609050	NXSI_039	912	34	89.5	425	5	DE359742	DE359742	WS00407.B2
840	34	89.5	384	3	BI981368	BI981368	fusi1h09.x	913	34	89.5	425	5	BU744284	BU744284	EST00007
841	34	89.5	384	9	AZ516325	AZ516325	RPCI-11-2	914	34	89.5	426	8	R88703	R88703	yp2d01.s
842	34	89.5	385	1	AI298019	AI298019	qm98502.x	915	34	89.5	426	9	AI214578	AI214578	SP-0019.B
843	34	89.5	387	1	AM339306	AM339306	hd72c05.x	916	34	89.5	428	1	AI090544	AI090544	qa64f01.x
844	34	89.5	387	2	BG450329	BG450329	NFO34H09D	917	34	89.5	428	5	BU060903	BU060903	UI-CF-FNO
845	34	89.5	388	1	AL640055	AL640055	AL640055	918	34	89.5	429	8	AZ150395	AZ150395	SP-0039.B
846	34	89.5	388	3	AM466154	AM466154	BP230022A	919	34	89.5	430	8	DR539950	DR539950	WS01026TB
847	34	89.5	389	1	BP817467	BP817467	BP817467	920	34	89.5	431	1	AI168041	AI168041	qz29g11.x
848	34	89.5	389	1	AA962180	AA962180	cm80d12.s	921	34	89.5	431	1	AI158132	AI158132	qw13f12.x
849	34	89.5	390	9	AQ931162	AQ931162	RPCI-23-2	922	34	89.5	431	2	BF092857	BF092857	MR4-TN011
850	34	89.5	391	5	BQ437926	BQ437926	AGENCOURT	923	34	89.5	431	2	BF740922	BF740922	QV1-HB003
851	34	89.5	391	9	AQ112478	AQ112478	CIT-HSP-2	924	34	89.5	431	6	CB359305	CB359305	ZF001-P00
852	34	89.5	394	1	AI023029	AI023029	cm65a07.s	925	34	89.5	432	1	AA709677	AA709677	vc15g07.x
853	34	89.5	394	1	AL843182	AL843182	AL843182	926	34	89.5	432	1	AM969754	AM969754	EST381832
854	34	89.5	396	1	AA674706	AA674706	vm74d12.s	927	34	89.5	432	8	H05285	H05285	yl18b07.s
855	34	89.5	396	9	AZ130628	AZ130628	OSUNB010	928	34	89.5	433	5	CA028090	CA028090	HZ60P10r
856	34	89.5	397	8	AA470635	AA470635	ne12c02.s	929	34	89.5	433	6	CB759491	CB759491	AMGNCUC.N
857	34	89.5	397	8	R45216	R45216	Y941d01.s	930	34	89.5	434	1	AA293425	AA293425	zc54b05.s
858	34	89.5	397	9	CC888836	CC888836	SALK_1524	931	34	89.5	434	1	AA619377	AA619377	vo87e11.x
859	34	89.5	399	5	BU734495	BU734495	UI-E-C11-	932	34	89.5	434	1	AQ169016	AQ169016	HS-3179.B
860	34	89.5	400	5	BY359715	BY359715	BY359715	933	34	89.5	435	1	AA483858	AA483858	ne76a07.s
861	34	89.5	401	6	CD285392	CD285392	G39163.39	934	34	89.5	436	1	AA808227	AA808227	oc40f10.s
862	34	89.5	401	9	CE096196	CE096196	l1gr-g8s-	935	34	89.5	436	6	CA636840	CA636840	w1e1n.pk0
863	34	89.5	401	10	CM650288	CM650288	OA_ABA019	936	34	89.5	436	7	CV626164	CV626164	zcno5902.
864	34	89.5	402	1	AL843710	AL843710	AL843710	937	34	89.5	436	8	W75988	W75988	zds5e07.r1
865	34	89.5	402	10	CZ532845	CZ532845	SRA-aac8	938	34	89.5	437	2	B2444909	B2444909	TCBAP1D26
866	34	89.5	403	1	AI269003	AI269003	qj67h10.x	939	34	89.5	437	3	BM145336	BM145336	TCAP1D47
867	34	89.5	404	1	AI500288	AI500288	tm94h11.x	940	34	89.5	437	3	BP685318	BP685318	BP685318
868	34	89.5	404	1	AA464732	AA464732	zx86a09.s	941	34	89.5	437	7	CN638845	CN638845	224A10_55
869	34	89.5	404	8	RG6410	RG6410	yh99b12.r1	942	34	89.5	437	9	B28879	B28879	T21H12TF
870	34	89.5	405	1	AV148190	AV148190	AV148190	943	34	89.5	438	1	AA039560	AA039560	zr70d09.s
871	34	89.5	405	1	BI832871	BI832871	603082440	944	34	89.5	438	9	B2350179	B2350179	hfs1c03.g
872	34	89.5	406	10	CL375634	CL375634	RPCI44.43	945	34	89.5	439	1	AA835673	AA835673	oc71g06.s
873	34	89.5	407	2	BF463393	BF463393	UI-M-CGP	946	34	89.5	439	1	AI130467	AI130467	qo54c01.x
874	34	89.5	407	2	BG055936	BG055936	na183d11.	947	34	89.5	440	2	BF529758	BF529758	602044025
875	34	89.5	407	6	CD196687	CD196687	MS1-0094G	948	34	89.5	440	5	BC037886	BC037886	dc69d05.y
876	34	89.5	408	1	AO549243	AO549243	RPCI-11-3	949	34	89.5	440	5	AX116312	AX116312	BX116312
877	34	89.5	408	2	BB800401	BB800401	BB800401	950	34	89.5	441	1	AI206707	AI206707	qf61a06.x
878	34	89.5	409	2	AA749353	AA749353	nx99f08.s	951	34	89.5	441	2	BB697992	BB697992	qf61a06.x
879	34	89.5	409	2	BB688282	BB688282	BB688282	952	34	89.5	441	9	B75773	B75773	RPCI11-12P1
880	34	89.5	410	2	BC091909	BC091909	mac18c11.	953	34	89.5	442	1	AA807711	AA807711	nm31f03.s
881	34	89.5	411	9	AQ683608	AQ683608	HS-5458_B	954	34	89.5	442	1	AM169667	AM169667	xj3f0f1.x
882	34	89.5	412	1	AI539593	AI539593	tp54a02.x	955	34	89.5	442	2	BF446970	BF446970	7066C06.x
883	34	89.5	412	8	N39166	N39166	yv26a07.s	956	34	89.5	442	8	P25096	P25096	HSPD11879.H
884	34	89.5	413	1	AA716177	AA716177	zg63g09.s	884	34	89.5	413	1	AA716177	AA716177	zg63g09.s
885	34	89.5	413	3	BP663093	BP663093	BP663093	885	34	89.5	413	3	BP663093	BP663093	BP663093
886	34	89.5	413	6	CA634743	CA634743	w1e1n.pk0	886	34	89.5	413	6	CA634743	CA634743	w1e1n.pk0
887	34	89.5	413	9	B2240464	B2240464	ch230-362	887	34	89.5	413	9	B2240464	B2240464	ch230-362
888	34	89.5	414	1	AI198843	AI198843	qf54g12.x	888	34	89.5	414	1	AI198843	AI198843	qf54g12.x
889	34	89.5	414	1	AM510448	AM510448	hbl5g04.x	889	34	89.5	414	1	AM510448	AM510448	hbl5g04.x
890	34	89.5	414	3	BM151177	BM151177	TCBAP1D13	890	34	89.5	414	3	BM151177	BM151177	TCBAP1D13
891	34	89.5	414												

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957 34 89.5 442 8 R28391
958 34 89.5 442 1 A0198860
959 34 89.5 443 1 A1824550
960 34 89.5 443 1 A0558451
961 34 89.5 443 1 BF150609
962 34 89.5 443 6 CB129727
963 34 89.5 443 6 CB129727
964 34 89.5 445 1 A0718693
965 34 89.5 445 8 DN891196
966 34 89.5 446 1 A1882881
967 34 89.5 446 1 A061536
968 34 89.5 446 1 A061536
969 34 89.5 446 5 BM468314
970 34 89.5 446 5 A0618393
971 34 89.5 447 3 B1746317
972 34 89.5 447 8 CX595238
973 34 89.5 447 10 CG666963
974 34 89.5 448 1 AA813141
975 34 89.5 449 1 A1801109
976 34 89.5 449 8 DN275077
977 34 89.5 450 3 BP390940
978 34 89.5 450 9 CC171695
979 34 89.5 450 10 CZ006461
980 34 89.5 452 1 AA393772
981 34 89.5 452 1 AA416667
982 34 89.5 453 8 H58239
983 34 89.5 453 9 CC797860
984 34 89.5 454 7 CK608155
985 34 89.5 454 7 CV038420
986 34 89.5 455 1 AA176512
987 34 89.5 456 1 AA839622
988 34 89.5 457 6 CB157839
989 34 89.5 458 1 A1364035
990 34 89.5 458 1 A1364035
991 34 89.5 458 1 AM370753
992 34 89.5 458 2 BE693523
993 34 89.5 458 3 BQ375018
994 34 89.5 458 9 BH122259
995 34 89.5 459 10 CL627310
996 34 89.5 460 9 AO912785
997 34 89.5 460 1 AA010337
998 34 89.5 461 1 AA933832
999 34 89.5 461 1 A1241834
1000 34 89.5 461 1 AA284051
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ALIGNMENTS

```
RESULT 1
LOCUS CRI96611/c 216 bp DNA linear GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPT insertion targeting and
chromosome engineering clone MHPN168n23, genomic survey sequence.
ACCESSION CRI96611.1 GI:49975460
VERSION CRI96611.1 GI:49975460
KEYWORDS GSS: genome survey sequence; MTCR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muria; Muridae; Murinae; Mus.
1 (bases 1 to 216)
AUTHORS Adams,D.J., Biggs,F.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonker,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,T. and Bradley,A.
JOURNAL Direct Submision
Submitted 20-FEB-2004 Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MTCR
FEATURES
source
1..216
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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US-10-757-745-2_COPY_115_121 (1-7) x CRI96611 (1-216)
ORIGIN
Alignment Scores:
Pred.: 1.29e+03 Length: 216
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0
QY 1 SerLeuileThrTPAsnile 7
|||||
DB 191 TCATTATATACCTGGATATTC 171
|||||
RESULT 2
LOCUS CR404572 221 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-872B08-026119,
genomic survey sequence.
ACCESSION CR404572.1 GI:46945300
VERSION CR404572.1 GI:46945300
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 Y. Y. Rosso, M.G., Strizhov, N., Viehovever, P. and Weisshaar, B.
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060
2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
3 Strizhov, N., Li, Y., Rosso, M.G., Viehovever, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 221)
Strizhov, N., Li, Y., Rosso, M.G. and Weisshaar, B.
Direct Submision
Submitted 01-MAY-2004 Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
MYF24. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated "GABI". Information on line availability can be found
at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
location/Qualifiers
1..221
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-872B08-026119"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
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/note="PCR was performed on DNA from *Arabidopsis thaliana* plants (11) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ37514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Alignment Scores:

Pred. No.:	1.32e+03	Length:	221
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CR0404572 (1-221)

QY

1 Serleuilethrttptanille 7
161 AGTTGATTAAGTGAACATA 181

RESULT 3

CR094068 227 bp DNA linear GSS 05-JUN-2004
Forward strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN414109, genomic survey sequence.

LOCUS

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	1.36e+03	Length:	227
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CR094068 (1-227)

QY

1 Serleuilethrttptanille 7
202 TCATTATTAACCTGAATATC 182

RESULT 4

CNS00VFS 246 bp DNA linear GSS 28-JUN-1999
Arabidopsis thaliana genome survey sequence Sp6 end of BAC T9H2 of TAMU library from strain Columbia of *Arabidopsis thaliana*, genomic survey sequence.

LOCUS

DEFINITION

ACCESSION

AL092207

VERSION AL092207.1 GI:5293361
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 246)
Salamonbat,M., Choise,N., Artiguenave,F., Brotier,P., Wincker,P., Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.

AUTHORS

JOURNAL

REFERENCES

AUTHORS

TITLE

JOURNAL

FEATURES

source

1.246
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="T9H2"
/clone_11b="TAMU"
/ecotype="Columbia"
/note="end : Sp6"

ORIGIN

Alignment Scores:

Pred. No.:	1.5e+03	Length:	246
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CNS00VFS (1-246)

QY

1 Serleuilethrttptanille 7
111 AGTTGATTAAGTGAACATA 91

RESULT 5

BB125347 289 bp mRNA linear EST 28-JUN-2000
LOCUS BB125347 RIKEN full-length enriched, 16 days neonate cerebellum Mus musculus cDNA clone 963004K16.3, similar to AF046001 Homo sapiens zinc finger transcription factor (ZNF207) mRNA, mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

Yoshitake Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenihiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-research.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoke, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.,
Thermolabile and thermostable activation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitanai, T., Akiyama, U., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.riken.go.jp) for further details.

FEATURES

Source

Location/Qualifiers

1..289
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9630004K16"
/tissue_type="cerebellum"
/dev_stage="16 days neonate"
/lab_host="DH10B"
/clone_1ib="RIKEN full-length enriched, 16 days neonate cerebellum"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATCTCCAGTAAATTAATTCACCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from lambda

ORIGIN

Alignment Scores:

Pred. No.: 1,82e+03 Length: 289
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BB125347 (1-289)

CY 1 Serleu1leThrTPaen1le 7

DB 83 TCTCTAATTACCTGGAATATC 63

RESULT 6

LOCUS

DEFINITION

ACCESSION

VERSION

T26956 310 bp mRNA linear EST 12-JUN-1996
11d155proj CloneTech adult human fat cell library H1108A Homo sapiens cDNA clone 11d155, mRNA sequence.
T26956 T27254
T26956.1 GI:575899

KEYWORDS
SOURCE
ORGANISM

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 310)
Boulland, P.
Study of expressed sequences tags in adipose tissue 1994
Unpublished (1994)
On Nov 17, 1994 this sequence version replaced gi:624970.
Contact: Frederic Boulland
Centre de Recherche sur l'Endocrinologie moleculaire et le Developpement
CNRS

FEATURES

Source

Location/Qualifiers

1..310
/organism="Homo sapiens"
/mol_type="mRNA"
/tissue="adipose"
/db_xref="taxon:9606"
/clone="11d155"
/clone_1ib="CloneTech adult human fat cell library H1108A"
/note="Vector: lambda g10; Site 1: EcoRI;
dev_stage=adult; tissue_type=adipose tissue;
lab_host=Escherichia coli; first strand priming with random and poly-d(T) oligonucleotides."

ORIGIN

Alignment Scores:

Pred. No.: 1,98e+03 Length: 310
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x T26956 (1-310)

CY 1 Serleu1leThrTPaen1le 7

DB 239 TCTCTAATTACCTGGAATATC 259

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BU070378/c 347 bp mRNA linear EST 27-AUG-2002
1m9c09.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6034553
3, similar to TR:095551 095551 DJ30M3.3 ;, mRNA sequence.
BU070378
BU070378.1 GI:22511567
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 347)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Maira, M., Pape, D., Wylie, T., Martin, J., Blaisdell, A., Schmidt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teegatschvili, R., Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 1m9c09.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochem.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco.

FEATURES

source

1..347
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6034553"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.:	2..26e+03	Length:	347
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU070378 (1-347)

QY 1 SerleuilemTTPASnile 7
|||||
51 TCTCTATTACCTGGAATATT 31

RESULT 8
LOCUS BQ787387 352 bp mRNA linear EST 26-JUL-2002
DEFINITION Im09c03.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE:6034553
VERSION BQ787387
KEYWORDS 5' similar to TR:O95551 O95551 DJ30M3.3 ; mRNA sequence.
SOURCE BQ787387.1 GI:2195859
EST
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 352)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemisha, I., Pearce, M., Bresnelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaras, V.,
Williams, T., Jackson, Y., and Bowers, Y.
Unpublished (2000)
Endocrine Pancreas Consortium

REFERENCE

AUTHORS

TITLE
JOURNAL
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochem.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco.

FEATURES

source

1..352
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6034553"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.:	2..3e+03	Length:	352
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BQ787387 (1-352)

QY 1 SerleuilemTTPASnile 7
|||||
298 TCTCTATTACCTGGAATATT 318

RESULT 9
LOCUS BE694706/c 368 bp mRNA linear EST 11-SEP-2000
DEFINITION PMO-BT0757-140800-006-d10 BT0757 Homo sapiens cDNA, mRNA sequence.
VERSION BE694706
KEYWORDS BE694706.1 GI:10081866
EST
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 368)
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsumura, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

REFERENCE

AUTHORS

TITLE
JOURNAL
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2707002
Fax: +55-11-2707001
Email: aaimpcon@iudwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.iudwig.org.br/scripte/gethtml2.pl?l=6&t2=PMO-B10757-140
800-006-d10c13-2000-08-14&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 37
High quality sequence stop: 368.
Location/Qualifiers
1..368
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/def_stage="Adult"
/clone_1fb="B10757"
/note="Organ: breast; Vector: puc18; Site 1: Sma1; Site 2: Sma2; A mini library was made by cloning products derived from GRESTES PCR (U.S. Patents Patent Application Number 196,716 - Ludwig Institute for Cancer Research) Profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	2.43e+03	Length:	368
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B10694706 (1-368)

QY 1 SerLeu11eHrTTPa11e 7
|||||

Db 266 TCTCTATTACTGGAAATATT 246

RESULT 10
LOCUS AV661333 394 bp mRNA linear EST 16-JAN-2002
DEFINITION AV661333 GLC Homo sapiens cDNA clone GLCGRD01 3', mRNA sequence.
ACCESSION AV661333
VERSION AV661333.1 GI:9882347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 394)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
11752456
JOURNAL
PUBMED
COMMENT
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..394

ORIGIN

Alignment Scores:

Pred. No.:	2.63e+03	Length:	394
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x AV661333 (1-394)

QY 1 SerLeu11eHrTTPa11e 7
|||||

Db 131 TCTCTATTACTGGAAATATT 151

RESULT 11
LOCUS B0582059 429 bp mRNA linear EST 20-JUN-2002
DEFINITION B0582059 Human insulinoma Homo sapiens cDNA clone IMAGE:6029589
5' similar to TR:095551 095551 D3J0M3.3', mRNA sequence.
ACCESSION B0582059
VERSION B0582059.1 GI:21494955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 429)
Wellton,D., Brown,J., Kenty,G., Remutt,A., Lee,C., Kaestner,K., Lemtink,I., Pearce,M., Bretzall,J., Gradowl,G., Clifton,S., Hillier,L., Marie,M., Pape,D., Wylie,T., Martin,J., Blissett,A., Schmitt,A., Treising,B., Nitter,B., Panko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,K., Cole,K., Teagardshvill,R., Williams,T., Jackson,I. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 1112c11.x1
Contact: Douglas Wellton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dwellton@molb.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Glbco.
Location/Qualifiers
1..429
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6029589"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1fb="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1: XhoI; Site 2: EcoRI; Constructed with lambda Zapri system

FEATURES
source

(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.:	2,916+03	Length:	429
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B0582059 (1-429)

Qy

1 SerleuilethrtTPAsnile 7
286 TCTCTCATTAACCTGGAATATT 306

RESULT 12

LOCUS

CR404571 457 bp DNA linear GSS 02-MAY-2004
Arabidopsis thaliana T-DNA flanking sequence GK-872B08-026084,
genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

CR404571.1 GI:46945299
GSS:
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE-

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

source

1. 457
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-872B08-026084"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Alignment Scores:

Pred. No.:	3,14e+03	Length:	457
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CR404571 (1-457)

Qy

1 SerleuilethrtTPAsnile 7
103 AGTTGATTACTTGGAACATA 123

RESULT 13

LOCUS

DN851694 463 bp mRNA linear EST 20-APR-2005
4147331 BARC 3GAL chicken mixed tissue Gallus gallus cDNA clone
3GAL 45109 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

Page 14

from whole brain, ultimobranchial gland, parathyroid gland, cecal tonsil and primordial germ cells Multiple"

ORIGIN

Alignment Scores:

Pred. No.:	3.19e+03	Length:	463
Score:	39.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x DN851694 (1-463)

QY 1 SerLeu1leThrTTrpAsnIle 7

Db 155 TCCTCATTTACCTGGAAATTT 175

RESULT 14

CR543841 471 bp mRNA linear EST 07-JUN-2004

LOCUS

DKFZP45900742.F1.459 (synonym: pcor1) Pongo pygmaeus CDNA clone

ACCESSION

DKFZP45900742.5, mRNA sequence.

VERSION

CR543841.1 GI:49895253

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	3.26e+03	Length:	471
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CR543841 (1-471)

QY 1 SerLeu1leThrTTrpAsnIle 7

Db 155 TCCTCATTTACCTGGAAATTT 175

RESULT 15

CR543841 471 bp mRNA linear EST 07-JUN-2004

LOCUS

DKFZP45900742.F1.459 (synonym: pcor1) Pongo pygmaeus CDNA clone

ACCESSION

DKFZP45900742.5, mRNA sequence.

Db 344 TCTTCATTTACCTGGAAATTT 364

RESULT 15

CB120234 473 bp mRNA linear EST 28-JAN-2003

LOCUS

K-EST0167337 LBSCKO Homo sapiens CDNA clone LBSCKO-29-F06 5', mRNA sequence.

ACCESSION

CB120234.1 GI:27946036

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	3.27e+03	Length:	473
Score:	39.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CB120234 (1-473)

QY 1 SerLeu1leThrTTrpAsnIle 7

Db 292 TCTTCATTTACCTGGAAATTT 312

RESULT 16

AT750554 480 bp mRNA linear EST 20-JUN-2002

LOCUS

U04401.Y1 Normal Human Trabecular Bone Cells Homo sapiens CDNA

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
Jia, J.B., Young, M.F., Touchman, J.W., Bouffard, G.G., Beckstrom-Sterberg, S.M., Green, E.D., Powell, J.I., Yang, L.M., Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.
SCAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
COMMENT
Contact: libin jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov

TITLE
JOURNAL
COMMENT

DNA sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).
Plate: 04 row: a column: 01
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers
1. .480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NHTRC-cn04a01"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
/clone_lib="Normal Human Trabecular Bone Cells"
/note="Organ: HIP; Vector: pBluescript; Site_1: EcoRI; Library constructed by Dr. Marian Young and Dr. Pamela Gehron Robey (NIDCR)"

FEATURES
source

ORIGIN

Alignment Scores:

Pred. No.: 3.3e+03 Length: 480
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AT50554 (1-480)

QY 1 SerLeuileThrTyrAsnile 7
|||||
337 TCTCTCATTCCTCGAATATT 357

Db 337 TCTCTCATTCCTCGAATATT 357

RESULT 17
AA486032 485 bp mRNA linear EST 06-MAR-1998
LOCUS ab40b10.r1 StrataGene Hela cell s3 937216 Homo sapiens cDNA clone
IMAGE:843259 5', mRNA sequence.

AA486032
AA486032.1 GI:2216248
EST.

ACCESSION
AA486032.1 GI:2216248
VERSION
AA486032.1 GI:2216248
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 485)
Hillier, L., Allen, M., Bowles, L., Dubugue, T., Geisler, G., Jost, S.,
Kritman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

TITLE
JOURNAL
COMMENT

Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: estw@wustl.edu

This clone is available royalty-free through LNC; contact the
IMAGS Consortium (info@image.lnl.gov) for further information.
Insert Length: 1913 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence scop: 444.
Location/Qualifiers
1. .485
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:843259"
/sex="Female"
/dev_stage="Hela S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene Hela cell s3 937216"
/note="Vector: pBluescript SK-; Site_1: EcoRI, Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. Hela S3
epithelioid carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; Uni-ZAP XR
Vector. ~5' adaptor sequence: 5' GAATTCGACGACG 3' ~3'
adaptor sequence: 5' CTCAGTTTTTTTTTTTTTTT 3"

FEATURES
source

ORIGIN

Alignment Scores:

Pred. No.: 3.37e+03 Length: 485
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AA486032 (1-485)

QY 1 SerLeuileThrTyrAsnile 7
|||||
333 TCTCTCATTCCTCGAATATT 353

Db 333 TCTCTCATTCCTCGAATATT 353

RESULT 18
BU659432 511 bp mRNA linear EST 30-SEP-2002
LOCUS c147f06.z1 Hembase; Erythroid Precursor Cells (UCB-cl library) Homo
BU659432
BU659432.1 GI:23371614
EST.

ACCESSION
BU659432.1 GI:23371614
VERSION
BU659432.1 GI:23371614
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 511)
Gubin, A.N., Lee, Y.T., Bouffard, G.G. and Miller, J.L.
Gene Expression in Human Erythroid Precursor Cells
Unpublished (2002)
Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jlmf@nih.gov

The 'cl' library was constructed by Alexander Gubin, Ph.D. in the
laboratory of Chemical Biology, NIDDK, NIH. DNA sequencing and/or
analyses by National Institutes of Health Intramural Sequencing
Center (NISC). More information available at:
http://hembase.nidk.nih.gov

Plate: 47 row: f column: 06
Seq primer: 5' lambda-TripLex2 Sequencing Primer.
Location/Qualifiers

TITLE
JOURNAL
COMMENT

FEATURES

source

```

1. 511
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="c147506"
/sex="unknown"
/tissue_type="blood"
/cell_line="Erythroid Precursor Cells"
/dev_stage="Primary Culture of Peripheral Blood Mononuclear Cells"
/lab_host="DH5alpha"
/clone_1ib="Hembase; Erythroid Precursor Cells (LCB:c1 library)"
/notes="Organ: blood; Vector: pTriplEx2; Site 1: SfiI; Site 2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/l peptide nucleic acid (PNA) oligos (N-terminal)-biotin-GTC-CAC-CCG-AGG-CTT-G-(C-terminal) and (N-terminal)-biotin-CTT-G-T-GAA-GTT-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC, Http://www.nisc.nih.gov/)."

```

ORIGIN

Alignment Scores:

```

Pred. No.: 3.59e+03 Length: 511
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

```

US-10-757-745-2_COPY_115_121 (1-7) x BU659432 (1-511)

```

QY 1 Serleu1ethrTTPanille 7
DB 30 TCATTCATTAACCTGGAATTA 10

```

```

RESULT 19 518 bp DNA linear GSS 25-APR-2003
CC153114
LOCUS CSU-K34.128K7.SP6.CSU-K34.Aedes aegypti genomic clone
DEFINITION CSU-K34.128K7, genomic survey sequence.
ACCESSION CC153114
VERSION CC153114.1 GI:30106410
KEYWORDS GSS
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
REFERENCE Nakayota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AUTHORS Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
TITLE Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
JOURNAL 1 (bases 1 to 518)
COMMENT 1 (bases 1 to 518)
BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other_GSS: CSU-K34.128K7.T7
Contact: Brendan Loftus
Department of Eukaryotic Genomics
MGR Medical Center Drive, Rockville, MD 20850, USA
712 301-838-3541
FAX: 301-838-0208
Email: bneale@ig.org
Library was provided by Susan Brown and Dennis Knudson at Colorado
State University.

```

```

Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1. 518
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/db_xref="taxon:7159"
/clone="CSU-K34.128K7"
/clone_1ib="CSU-K34"
/notes="Vector: pBAC3.6; Site 1: EcoRI; Source DNA: Aedes aegypti; strain unknown (derived from freshly hatched larvae at the Virus Research Centre, Poona, India. Reference: SINGH, K. R. P., 1967 Cell cultures derived from larvae of Aedes albopictus (Skuse) and Aedes aegypti (L.). Current Science 36: 506-508); ATC-10 cell line ATCC CCL-125"

```

ORIGIN

Alignment Scores:

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Pred. No.: 3.65e+03 Length: 518
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

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US-10-757-745-2_COPY_115_121 (1-7) x CC153114 (1-518)

```

QY 1 Serleu1ethrTTPanille 7
DB 167 TCCTCATTAACCTGGAACAT 187

```

```

RESULT 20 530 bp mRNA linear EST 06-MAR-2002
BM646221
LOCUS K-EST0125204.S13KMS5 Homo sapiens cDNA clone S13KMS5-59-C04 5',
DEFINITION mRNA sequence.
ACCESSION BM646221
VERSION BM646221.1 GI:19202620
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
1 (bases 1 to 530)
21C Frontiers Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@kribb.re.kr
Plate: 59 row C column: 04
High quality sequence stop: 530.
Location/Qualifiers
1 530
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-59-C04"
/tissue_type="myeloma"
/cell_line="RMS-5"
/lab_host="TOP10F"
/clone_1ib="S13KMS5"
/notes="Vector: pCNS; Site 1: BcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacapped with tobacco acid

```

Library was provided by Susan Brown and Dennis Knudson at Colorado State University.

pyrophosphatase (TAP). The deprotected intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.:	3.75e+03	Length:	530
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BM646221 (1-530)

QY 1 SerLeu11eThrTTPan1le 7

DB 347 TCTCTCATTAACCTGGAATATT 367

RESULT 21

LOCUS CN233559 531 bp mRNA linear EST 09-APR-2004
 DEFINITION RJA113F02.ab1 Rbubrain Gallus gallus cDNA 5', mRNA sequence.
 ACCESSION CN233559
 VERSION CN233559.1 GI:46337303
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; 1 (bases 1 to 531)
 Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and Lundberg, U.
 EST analysis of brain and testis cDNA libraries from White Leghorn and Red Jungle Fowl
 Unpublished (2004)
 CONTACT: Peter Savolainen
 Department of Biotechnology
 Royal Institute of Technology, KTH
 SE-106 91 Stockholm, SWEDEN
 Tel: +46 (0)8 5537 8481
 Fax: +46 (0)8 5537 8335
 Email: Peter.Savolainen@biotech.kth.se
 Seq primer: M13 reverse primer.
 Location/Qualifiers
 1..531
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Red junglefowl"
 /db_xref="taxon:9031"
 /sex="female"
 /lab_host="Electromax DH10B (Invitrogen)"
 /clone_lib="Rbubrain"
 /note="Organ: Brain; Vector: pSPORT-1; Site 1: Hind III, Site 2: EcoRI; The cDNA libraries were created with the Superscript Plasmid System (Invitrogen)."

ORIGIN
 Alignment Scores:
 Pred. No.: 3.76e+03 Length: 531
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Mismatches: 0
 Conservative: 0

JOURNAL
 COMMENT

FEATURES
 source

ORIGIN

Alignment Scores:

Pred. No.: 3.76e+03 Length: 531
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Mismatches: 0
 Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN233559 (1-531)

QY 1 SerLeu11eThrTTPan1le 7

DB 303 TCGTCGATTAACCTGGAACATT 323

RESULT 22

LOCUS BP220985 554 bp mRNA linear EST 15-SEP-2004
 DEFINITION BP220985 Sugano cDNA library, colon Homo sapiens cDNA clone COL06450, mRNA sequence.
 ACCESSION BP220985
 VERSION BP220985.1 GI:52093890
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo
 1 (bases 1 to 554)
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)
 15342556
 CONTACT: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 106-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers
 1..554
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="COL06450"
 /tissue_type="colon"
 /clone_lib="Sugano cDNA library, colon"

JOURNAL
 COMMENT

FEATURES
 source

ORIGIN
 Alignment Scores:
 Pred. No.: 3.95e+03 Length: 554
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP220985 (1-554)

QY 1 SerLeu11eThrTTPan1le 7

DB 252 TCTCTCATTAACCTGGAATATT 272

RESULT 23

LOCUS BX997515/c 558 bp DNA linear GSS 05-UTL-2004
 DEFINITION BX997515 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone WHP34112, genomic survey sequence.
 ACCESSION BX997515
 VERSION BX997515.1 GI:49728973
 KEYWORDS GSS; genome survey sequence; MICR.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 1 (bases 1 to 558)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

```

AUTHORS      Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
              Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
              Rogers,J. and Bradley,A.
TITLE        Direct Submission
JOURNAL      Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
              CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES
  source
    1..558
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      /clone_1fb="MHP"
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Alignment Scores:
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  Percent Similarity: 100.0%     Conservative: 0
  Best Local Similarity: 100.0%  Mismatches: 0
  Query Match:    100.0%        Indels:      0
  DB:             10            Gaps:         0
US-10-757-745-2_COPY_115_121 (1-7) x BX997515 (1-558)
QY
  Db      1 Serleu1eThrTpAsn1le 7
          472 TCCTGATTACTTGGAATATT 452
RESULT 24
LOCUS     BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
DEFINITION
  BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
  clone DMC03190, mRNA sequence.
ACCESSION
  BP226620
  BP226620.1 GI:52099525
VERSION   EST.
KEYWORDS
  SOURCE   Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homiidae; Homo.
  1 (bases 1 to 565)
  Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
  Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  Sequence comparison of human and mouse genes reveals a homologous
  block structure in the promoter regions
  Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL   PUBMED
  15342556
  Contact: Yutaka Suzuki
  Department of Virology
  Institute of Medical Science, University of Tokyo
  4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
  Email: ysuzuki@ims.u-tokyo.ac.jp.
  Location/Qualifiers
FEATURES
  source
    1..565
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      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone_1fb="DMC03190"
      /clone_1fb="Sugano cDNA library, dermoid cancer"
      /note="dermoid cancer"
ORIGIN
Alignment Scores:
  Pred. No.:      4,056+03      Length:      565
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  Percent Similarity: 100.0%     Conservative: 0
  Best Local Similarity: 100.0%  Mismatches: 0
  Query Match:    100.0%        Indels:      0
  DB:             3            Gaps:         0
US-10-757-745-2_COPY_115_121 (1-7) x BP226620 (1-565)
US-10-757-745-2_COPY_115_121 (1-7) x BP220508 (1-566)
QY
  Db      1 Serleu1eThrTpAsn1le 7
          262 TCCTCATTCCTCGAATATT 282
RESULT 26
LOCUS     BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone
DEFINITION
  BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone
  HRK00430, mRNA sequence.
ACCESSION
  BP257211
  BP257211.1 GI:52172441
VERSION   EST.
KEYWORDS
  SOURCE   Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homiidae; Homo.
  1 (bases 1 to 568)
  Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
  Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  Sequence comparison of human and mouse genes reveals a homologous
  block structure in the promoter regions
  Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL
```

PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1. 568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRT00430"
/tissue_type="heart"
/clone_lib="Sugano cDNA library, heart"
ORIGIN
Alignment Scores:
Pred. No.: 4.07e+03 Length: 568
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BP257211 (1-568)
QY 1 SerLeu1leThrTrpAsnIle 7
DB 313 TCTCTCATTAACCTGGAATATT 333
RESULT 27
LOCUS BM172060 570 bp mRNA linear EST 04-DEC-2001
DEFINITION IMAGE3_3-2001/bm1293bdf41.xl NIH_MGC_76 Homo sapiens cDNA clone
ACCESSION BM172060 IMAGE:4700059 5', mRNA sequence.
VERSION BM172060.1 GI:17311623
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 570)
Kale, P.I., Harech, T.J., Folta, P.A., Nelson, D.O., Sanders, C.G. and
Prange, C.K.
The I.M.A.G.E. Consortium quality control effort: clone
ressequencing for verification
Unpublished (2001)
Other ESTs: BG533717
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the
correct orientation), as part of the I.M.A.G.E. Consortium quality
control effort. High quality sequence is defined as having 100 or
more base pairs with a phred quality value of 20 or greater, where
a sliding window of 4 base pairs with a phred quality value of 15
or greater marks the beginning and end of the sequence. For
information on obtaining this clone, please contact
info@image.llnl.gov.
Plate: LHCMI533 Row: a Column: 20
Seq primer: -21m13
High quality sequence stop: 570.
Location/Qualifiers
1. 570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4700059"
/lab_host="DH10B (T1 phage-resistant) "

/clone_lib="NIH_MGC_76"
/note="Organ: liver; Vector: pDNR-L1B (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggccatratgcc); 5'-and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCGCATTTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 4.09e+03 Length: 570
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BM172060 (1-570)
QY 1 SerLeu1leThrTrpAsnIle 7
DB 195 TCTCTCATTAACCTGGAATATT 215
RESULT 28
LOCUS BP221518 570 bp mRNA linear EST 15-SEP-2004
DEFINITION BP221518 Sugano cDNA library, colon Homo sapiens cDNA clone
ACCESSION COL09203, mRNA sequence.
VERSION BP221518
KEYWORDS BP221518.1 GI:52094423
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 570)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1. 570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL09203"
/tissue_type="colon"
/clone_lib="Sugano cDNA library, colon"
ORIGIN
Alignment Scores:
Pred. No.: 4.09e+03 Length: 570
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BP221518 (1-570)
QY 1 SerLeu1leThrTrpAsnIle 7

```

Db          251 TCTCATTAACCTGGAAATATT 271
|||||
RESULT 29   BU397611 570 bp mRNA linear EST 27-NOV-2002
LOCUS       BU397611
DEFINITION  603534313F1 CSEQCCHN58 Gallus gallus cDNA clone CHEST493j4 5', mRNA
sequence.
ACCESSION   BU397611
VERSION     BU397611.1
KEYWORDS    GI:25766654
SOURCE      EST
ORGANISM    Gallus gallus (chicken)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 570)
REFERENCE   Boardman, P.B., Sanz-Bizquerro, J., Overton, I.M., Burt, D.W., Boesch, E.,
AUTHORS     Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE       A Comprehensive Collection of Chicken cDNAs
JOURNAL     Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED     12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612068930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
            Location/Qualifiers
            1..570
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /strain="Compton Line 151"
            /db_xref="taxon:9031"
            /clone="CHST493j4"
            /sex="Female"
            /day_stage="adult"
            /lab_host="DH10B"
            /clone_lib="CSEQCCHN58"
            /note="Organ: small intestine; Vector: pBluescript II
            KS(+); Site: 1. EcoRI; Site 2: NotI; This normalized
            library was constructed from 1 million independent clones.
            cDNA synthesis was initiated using an oligo(dT) primer,
            using methylated C in the first strand synthesis reaction.
            Following this, first strand reaction, double-stranded cDNA
            was blunt-ended, ligated to NotI adapters, digested with
            EcoRI, size-selected, and cloned into the NotI and EcoRI
            compatible sites of a custom modified MCS of the
            pBluescript (KS) vector. The library was normalized in 2
            rounds using conditions adapted from Soares et al., PNAS
            (1984) 81:9228-9232 and Bonaldo et al., Genome Research 6
            (1996) 791, except that a significantly longer
            reannealing hybridization was used."
ORIGIN
Alignment Scores:
Pred. No.: 4.09e+03 Length: 570
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BU397611 (1-570)
QY          1 SerLeuIIeHnTTPaenIIe 7
DB          80 TCGTGATTAACCTGGAAATATT 100
RESULT 30   BP262485
BP262485

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```

LOCUS       BP262485 572 bp mRNA linear EST 16-SEP-2004
DEFINITION  BP262485 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS107111, mRNA sequence.
ACCESSION   BP262485
VERSION     BP262485.1
KEYWORDS    GI:52177716
SOURCE      EST
ORGANISM    Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 572)
REFERENCE   Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
AUTHORS     Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE       Sequence comparison of human and mouse genes reveals a homologous
JOURNAL     block structure in the promoter regions
PUBMED     Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp.
            Location/Qualifiers
            1..572
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="HS107111"
            /tissue_type="small intestine"
            /clone_lib="Sugano cDNA library, small intestine"
ORIGIN
Alignment Scores:
Pred. No.: 4.11e+03 Length: 572
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BP262485 (1-572)
QY          1 SerLeuIIeHnTTPaenIIe 7
DB          299 TCTCATTAACCTGGAAATATT 319
RESULT 31   AU279894 573 bp mRNA linear EST 31-JUL-2003
LOCUS       AU279894
DEFINITION  AU279894 CHONS2 Homo sapiens cDNA clone CHONS2002038 5', mRNA
sequence.
ACCESSION   AU279894
VERSION     AU279894.1
KEYWORDS    GI:28299121
SOURCE      EST
ORGANISM    Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 573)
REFERENCE   Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R.,
AUTHORS     Isegai, T., Hara, J., Tomoya, Y. and Umesawa, A.
TITLE       Redifferentiation of dedifferentiated chondrocytes and
JOURNAL     chondrogenesis of human bone marrow stromal cells via chondrosphere
PUBMED     formation with expression profiling by large-scale cDNA analysis
            Exp. Cell Res. 288 (1), 35-50 (2003)
            12876157
COMMENT     Contact: Takao Isegai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975

```


Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA Project, Sugiyama, T.; Wakamatsu, A.; Irie, R.;
Umezawa, A.; Fukuma, M.; Kuwakari, S.; Hata, J.; Ishii, S.; Yamamoto, J.;
Isono, Y.; Saito, K.; Nakamura, Y.; Masuko, Y.; Nagai, K.; Isogai, T.
HRI human cDNA Project: cDNA library construction & 5'-end one
pass sequencing: Helix Research Institute.

FEATURES
source
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ORIGIN

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Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AU279894 (1-573)

QY
1 SerLeuileThrTrpAsnIle 7
|||||
380 TCTCTCATTAACCTGGAAATATT 400

RESULT 32
BP221260 573 bp mRNA linear EST 15-SEP-2004
LOCUS BP221260 Sugano cDNA library, colon Homo sapiens cDNA clone
DEFINITION COL08083, mRNA sequence.
ACCESSION BP221260
VERSION BP221260.1 GI:52094165
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 573)
Score: 4.12e+03 Length: 573
Percent Similarity: 100.0% Matches: 7
Best Local Similarity: 100.0% Conservative: 0
Query Match: 100.0% Mismatches: 0
Indels: 0
Gaps: 0

JOURNAL
PUBMED
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 4.12e+03 Length: 573
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Percent Similarity: 100.0% Conservative: 0
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Query Match: 100.0% Indels: 0
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DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP221260 (1-573)

QY
1 SerLeuileThrTrpAsnIle 7
|||||
265 TCTCTCATTAACCTGGAAATATT 285

RESULT 33
BP261500 573 bp mRNA linear EST 16-SEP-2004
LOCUS BP261500 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS103816, mRNA sequence.
ACCESSION BP261500
VERSION BP261500.1 GI:52176731
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 573)
Score: 4.12e+03 Length: 573
Percent Similarity: 100.0% Matches: 7
Best Local Similarity: 100.0% Conservative: 0
Query Match: 100.0% Mismatches: 0
Indels: 0
Gaps: 0

JOURNAL
PUBMED
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/issue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 4.12e+03 Length: 573
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP261500 (1-573)

QY
1 SerLeuileThrTrpAsnIle 7
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249 TCTCTCATTAACCTGGAAATATT 269

RESULT 34
BP262642 576 bp mRNA linear EST 16-SEP-2004
LOCUS BP262642 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS107584, mRNA sequence.
ACCESSION BP262642
VERSION BP262642.1 GI:52177873
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 576)
Score: 4.12e+03 Length: 576
Percent Similarity: 100.0% Matches: 7
Best Local Similarity: 100.0% Conservative: 0
Query Match: 100.0% Mismatches: 0
Indels: 0
Gaps: 0

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

Page 22

TITLE
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)

PUBMED
15342556

COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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ORIGIN

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Query Match: 100.0% Indels: 0
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US-10-757-745-2_COPY_115_121 (1-7) x BP262642 (1-576)

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267 TCTCTCATTTACCTGGATATTT 287

RESULT 35
CN298919 577 bp mRNA linear EST 16-MAY-2004
LOCUS
17000600175228 GRN_PRRHP Homo sapiens cDNA 5', mRNA sequence.
CN298919.1 GI:47315333
EST
CN298919.1 GI:47315333
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 577)
Branderger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, J., Wang, R., Guejter, K., Rao, M.S., Mandalam, R.,
Lebowitz, J. and Stenou, L.,
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
CONTACT: Branderger R
Regenerative Medicine
Seron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 9658
Fax: 650 473 9760
Email: rbranderger@seron.com
Location/Qualifiers
Insert Length: 577 Std Error: 0.00.
Location/Qualifiers
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line"
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/note="oligo dT primed, full-length enriched cDNA library
from DMSO-treated H9 cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 4.15e+03 Length: 577
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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US-10-757-745-2_COPY_115_121 (1-7) x CN298919 (1-577)

QY
1 SerleuileThrTPanile 7
|||||
343 TCTCTCATTTACCTGGATATTT 363

RESULT 36
BP261787 580 bp mRNA linear EST 16-SEP-2004
BP261787
LOCUS
BP261787 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS105008, mRNA sequence.
DEFINITION
BP261787
BP261787
BP261787
BP261787.1 GI:52177018
EST
CN298919.1 GI:52177018
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 580)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 4.18e+03 Length: 580
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Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP261787 (1-580)

QY
1 SerleuileThrTPanile 7
|||||
278 TCTCTCATTTACCTGGATATTT 298

RESULT 37
BP274368 580 bp mRNA linear EST 16-SEP-2004
BP274368
LOCUS
BP274368 Sugano cDNA library, kidney Homo sapiens cDNA clone
KDN00894, mRNA sequence.
DEFINITION
BP274368
BP274368
BP274368
BP274368.1 GI:52188100
EST
CN298919.1 GI:52188100
KEYWORDS
SOURCE
Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 580)
 Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J., Mizushima-Sugano.S., Nakai.K. and Sugano.S.
 Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004).

JOURNAL PUBMED 15342556
 CONTACT: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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 1..580
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ORIGIN
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 Percent Similarity: 100.0% Conservative: 0
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 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP274368 (1-580)

QY 1 SerLeuIleThrTPAsnIle 7
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Db 363 TCTCTCATTCCTGGAAATATT 383

RESULT 38
 AV1717253 581 bp mRNA linear EST 16-OCT-2000
 LOCUS AV1717253 DDB Homo sapiens cDNA clone DCBMA04 5', mRNA sequence.
 ACCESSION AV1717253
 VERSION AV1717253.1 GI:10814405
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 581)
 Xu.X., Gu.J., Liu.F., Qu.J., Zhao.M., Li.Y., Huang.Q., Zhou.J., Song.H., Gu.Y., Yang.Y., Gao.G., Xiao.H., Li.N., Qian.B., Gao.X., Cheng.Z., Xu.S., Gu.W., Tu.Y., Jia.J., Fu.G., Ren.S., Zhong.M., Lu.G., Cheng.Z., and Han.Z.
 Homo sapiens cDNA DCB clones
 Unpublished (2000)
 CONTACT: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
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 /db_xref="taxon:9606"
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US-10-757-745-2_COPY_115_121 (1-7) x BP199948 (1-581)

QY 1 SerLeuIleThrTPAsnIle 7
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Db 379 TCTCTCATTCCTGGAAATATT 399

RESULT 40
 BP207751 581 bp mRNA linear EST 14-SEP-2004
 LOCUS BP207751

REFERENCE 1 (bases 1 to 581)
 Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J., Mizushima-Sugano.S., Nakai.K. and Sugano.S.
 Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL PUBMED 15342556
 CONTACT: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

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DEFINITION BP207751 Sugano cDNA library, coronary artery smooth muscle cell
ACCESSION BP207751
VERSION BP207751.1 GI:52064157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
            Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp.

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Score: 38.00 Matches: 7
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP207751 (1-581)

QY 1 SerleuileThrTyrPasnile 7
Db 251 TCTCTCATTTACCTGGAAATATT 271

RESULT 41
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LOCUS BP225088 Sugano cDNA library, lymphocyte Daudi Homo sapiens cDNA
DEFINITION clnt3 DAT05184, mRNA sequence.
ACCESSION BP225088
VERSION BP225088.1 GI:5207993
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
            Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp.

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    /note="Burkitt's lymphoma"

ORIGIN
Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP225088 (1-581)

QY 1 SerleuileThrTyrPasnile 7
Db 364 TCTCTCATTTACCTGGAAATATT 384

RESULT 42
BP262638 581 bp mRNA linear EST 16-SEP-2004
LOCUS BP262638 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS107576, mRNA sequence.
ACCESSION BP262638
VERSION BP262638.1 GI:52177869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
            Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp.

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        /clone_lib="Sugano cDNA library, small intestine"

ORIGIN
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP262638 (1-581)

QY 1 SerleuileThrTyrPasnile 7

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Db 260 TCCTCATTTACCTGGAATATT 280

RESULT 43
LOCUS BP264149
DEFINITION BP264149 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS114850, mRNA sequence.
ACCESSION BP264149.1 GI:52179380
VERSION BP264149.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP264149 (1-581)

QY 1 SerLeuIleThrTrpAsnIle 7
|||||
Db 309 TCCTCATTTACCTGGAATATT 329

RESULT 44
LOCUS BP270744
DEFINITION BP270744 Sugano cDNA library, small intestine Homo sapiens cDNA
clone KAR05146, mRNA sequence.
ACCESSION BP270744
VERSION BP270744.1 GI:52220093
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology

FEATURES
source 1..581
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/clone="KAR05146"
/issue_type="small intestine"
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ORIGIN
Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP349936 (1-581)

QY 1 SerLeuIleThrTrpAsnIle 7
|||||
Db 251 TCCTCATTTACCTGGAATATT 271

RESULT 45
LOCUS BP349936
DEFINITION BP349936 Sugano cDNA library, brain Homo sapiens cDNA clone
SZR06923, mRNA sequence.
ACCESSION BP349936
VERSION BP349936.1 GI:52279921
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SZR06923"
/issue_type="brain"
/clone_lib="Sugano cDNA library, brain"

ORIGIN
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Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP349936 (1-581)

QY 1 SerLeuIleThrTrpAsnIle 7

DB 120 TCTCTCATTTACCTGGAAATATT 140

RESULT 46
BP379659
LOCUS
DEFINITION BP379659 Sugano cDNA library, uterus Homo sapiens cDNA clone
WMD06642. mRNA sequence.

ACCESSION BP379659
VERSION BP379659.1 GI:52412762
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 581)
Suzuki Y., Yamashita R., Shiota M., Sakakibara Y., Chiba J.,
Mizushima-Sugano J., Nakai K. and Sugano S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED
COMMENT
CONTACT: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzaki@iim.u-tokyo.ac.jp

FEATURES
source
1..581 sm="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="WMD0642"
/tissue_type="uterus"
/clone_lib="Sugano cDNA library, uterus"

ORIGIN

Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP379659 (1-581)

QY 1 SerLeuIleThrTPanille 7
DB 252 TCTCTCATTTACCTGGAAATATT 272

RESULT 47
BM507091
LOCUS
DEFINITION BM507091 582 bp mRNA linear EST 15-FEB-2002
1h24h01.y1 Human Insulinoma Homo sapiens cDNA 5' similar to
TR:095551 O95551 D030W3.3, mRNA sequence.

ACCESSION BM507091
VERSION BM507091.1 GI:18678234
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 582)
Melton D., Brown J., Kenty G., Permutt A., Lee C., Kaestner K.,
Hillier L., Marra M., Pape D., Wylie T., Martin J., Birstein A.,
Schmitt A., Theising B., Ritzer E., Ronko T., Bennett J.,
Cardenas M., Gibbons M., McCann R., Cole R., Tsagaris V., R.,
Williams T., Jackson Y. and Bowers Y.
Endocrine Pancreas Consortium

REFERENCE
AUTHORS

JOURNAL
PUBMED
COMMENT

JOURNAL
COMMENT
Unpublished (2000)
Other ESTs: 1h24h01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochem.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBlueScript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from G1bco
High quality sequence stop: 269.

FEATURES
source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/notes="Organ: pancreas; Vector: pBlueScript SK-; Site: 1;
XhoI; Site 2: EcoRI; Constructed with lambda ZAPIT system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBlueScript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:
Pred. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BM507091 (1-582)

QY 1 SerLeuIleThrTPanille 7
DB 145 TCTCTCATTTACCTGGAAATATT 165

RESULT 48
BP219740
LOCUS
DEFINITION BP219740 Sugano cDNA library, caudate nucleus Homo sapiens cDNA
clone CNR08985, mRNA sequence.

ACCESSION BP219740
VERSION BP219740.1 GI:52092643
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 582)
Suzuki Y., Yamashita R., Shiota M., Sakakibara Y., Chiba J.,
Mizushima-Sugano J., Nakai K. and Sugano S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

REFERENCE
AUTHORS

JOURNAL
PUBMED
COMMENT
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1.582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NC08985"
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/clone_lib="Sugano cDNA library, caudate nucleus"

ORIGIN

Alignment Scores:

Pred. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP219740 (1-582)

QY 1 SerLeuIleThrTrpAsnIle 7

DB 358 TCTCTCATTAACCTGGAAATATT 378

RESULT 49

BP233592 582 bp mRNA linear EST 15-SEP-2004
LOCUS BP233592 Sugano cDNA library, coronary artery endothelial cell Homo
DEFINITION sapiens cDNA clone HCR0774, mRNA sequence.
ACCESSION BP233592 GI:52106502
VERSION BP233592.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
1 (bases 1 to 582)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

TITLE

JOURNAL Mizushima-Sugano,J., Nakai,K. and Sugano,S.
PUBMED Sequence comparison of human and mouse genes reveals a homologous
15342556 block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

COMMENT

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Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1.582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR0774"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_lib="Sugano cDNA library, coronary artery
endothelial cell"

ORIGIN

Alignment Scores:

Pred. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP233592 (1-582)

QY 1 SerLeuIleThrTrpAsnIle 7
DB 358 TCTCTCATTAACCTGGAAATATT 378

RESULT 50

BP234218 582 bp mRNA linear EST 15-SEP-2004
LOCUS BP234218 Sugano cDNA library, coronary artery endothelial cell Homo
DEFINITION sapiens cDNA clone HCR02378, mRNA sequence.
ACCESSION BP234218 GI:52107128
VERSION BP234218.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
1 (bases 1 to 582)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

TITLE

JOURNAL Mizushima-Sugano,J., Nakai,K. and Sugano,S.
PUBMED Sequence comparison of human and mouse genes reveals a homologous
15342556 block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

COMMENT

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Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1.582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR02378"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_lib="Sugano cDNA library, coronary artery
endothelial cell"

ORIGIN

Alignment Scores:

Pred. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP234218 (1-582)

QY 1 SerLeuIleThrTrpAsnIle 7

DB 370 TCTCTCATTAACCTGGAAATATT 390

RESULT 51

BP261141 582 bp mRNA linear EST 16-SEP-2004
LOCUS BP261141 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS102606, mRNA sequence.
ACCESSION BP261141 GI:52176372
VERSION BP261141.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
1 (bases 1 to 582)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

TITLE Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions
JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)
15342556
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..582
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/mol_type="mRNA"
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ORIGIN
Alignment Scores:
Prod. No.: 4.19e+03 Length: 582
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP261141 (1-582)

Qy 1 SerleuilethrtPpanille 7
|||||
Db 249 TCTCTCATTACCTCGAATATT 269

RESULT 52
BP263516 582 bp mRNA linear EST 16-SEP-2004
LOCUS
DEFINITION
BP263516 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS11929, mRNA sequence.

ACCESSION
BP263516
VERSION
BP263516.1 GI:521878747
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED
COMMENT
Contact: Yutaka Suzuki
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..582
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/mol_type="mRNA"
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/clone="HS11929"
/issue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN
Alignment Scores:
Prod. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP270415 (1-582)

Qy 1 SerleuilethrtPpanille 7
|||||
Db 341 TCTCTCATTACCTCGAATATT 361

RESULT 54
BP275810 582 bp mRNA linear EST 16-SEP-2004
LOCUS
DEFINITION
BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone
KD04583, mRNA sequence.

ACCESSION
BP275810
VERSION
BP275810.1 GI:52189542
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.

block structure in the promoter regions
JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)
15342556
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
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ORIGIN
Alignment Scores:
Prod. No.: 4.19e+03 Length: 582
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP270415 (1-582)

Qy 1 SerleuilethrtPpanille 7
|||||
Db 341 TCTCTCATTACCTCGAATATT 361

RESULT 54
BP275810 582 bp mRNA linear EST 17-SEP-2004
LOCUS
DEFINITION
BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone
KD04583, mRNA sequence.

ACCESSION
BP275810
VERSION
BP275810.1 GI:52189542
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. 582
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="KDN04583"
/tissue_type="kidney"
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ORIGIN

Alignment Scores:

Pred. No.:	4.19e+03	Length:	582
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BP275810 (1-582)

Qy 1 SerLeuIleThrTyrAsnIle 7
|||||
Db 332 TCTCTCATTAAGCTGGAATATT 352

RESULT 55
BP195721 583 bp mRNA linear EST 14-SEP-2004
LOCUS BP195721 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION ADB08961, mRNA sequence.
ACCESSION BP195721
VERSION BP195721.1 GI:52039998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. 583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADB08961"
/tissue_type="brain"
/clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:

Pred. No.:	4.2e+03	Length:	583
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	100.0%	Mismatches:	0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP195721 (1-583)

Qy 1 SerLeuIleThrTyrAsnIle 7
|||||
Db 400 TCTCTCATTAAGCTGGAATATT 420

RESULT 56
BP262103 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS105902, mRNA sequence.
ACCESSION BP262103
VERSION BP262103.1 GI:52177334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. 583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS105902"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:

Pred. No.:	4.2e+03	Length:	583
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BP262103 (1-583)

Qy 1 SerLeuIleThrTyrAsnIle 7
|||||
Db 277 TCTCTCATTAAGCTGGAATATT 297

RESULT 57
BP262741 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP262741 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS107919, mRNA sequence.
ACCESSION BP262741
VERSION BP262741.1 GI:52177972
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

TITLE Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
 source
 1..583
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HS107919"
 /issue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"
ORIGIN
 Alignment Scores:
 Pred. No.: 4.2e+03 Length: 583
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Mismatches: 0
 Best Local Similarity: 100.0% Indels: 0
 Query Match: 100.0% Gaps: 0
 DB: 3
 US-10-757-745-2_COPY_115_121 (1-7) x BP262741 (1-583)
 QY 1 SerLeuIleThrTPaenlle 7
 DB 213 TCTCTACTTACCTGGAAATATT 233
RESULT 58 BP319548 583 bp mRNA linear EST 17-SEP-2004
LOCUS BP319548 Sugano cDNA library, pericardium Homo sapiens cDNA clone
DEFINITION FCD11128, mRNA sequence.
ACCESSION BP319548
VERSION BP319548.1 GI:52248523
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo
 1 (bases 1 to 583)
 Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
 source
 1..583
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="FCD11128"
 /issue_type="pericardium"
 /clone_lib="Sugano cDNA library, pericardium"
ORIGIN
 Alignment Scores:
 Pred. No.: 4.2e+03 Length: 583
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Mismatches: 0
 Best Local Similarity: 100.0% Indels: 0
 Query Match: 100.0% Gaps: 0
 DB: 3
 US-10-757-745-2_COPY_115_121 (1-7) x BP319548 (1-583)
 QY 1 SerLeuIleThrTPaenlle 7
 DB 392 TCTCTACTTACCTGGAAATATT 412
RESULT 59 BP783229 583 bp mRNA linear EST 11-OCT-2002
LOCUS BP783229
DEFINITION In01a08.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6123158
 5' similar to TR:095551 O95551 DJ30M3.3 ;, mRNA sequence.
ACCESSION BP783229
VERSION BP783229.1 GI:23827207
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 583)
 Melton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Bilezikian,A.,
 Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J.,
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvill,I.,R.,
 Williams,T., Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: in01a08.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohpc.harvard.edu
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 Bluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 430.
FEATURES
 source
 1..583
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6123158"
 /issue_type="insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Human insulinoma"
 /note="Organ: pancreas; Vector: Bluescript SK-; Site: 1:
 XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 Bluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/eat/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further
 information on this library (Metabolism Division, Permut
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas EST project library."

Best Local Similarity: 100.0%
 Query Match: 100.0%
 DB: 5
 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU783229 (1-583)

QY 1 SerleulleThrTpAsnIle 7
 DB 341 TCTCTCATTAACCTGGAAATATT 361

RESULT 60
 BP263059
 LOCUS BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA
 ACCESSION BP263059
 VERSION BP263059.1 GI:52178290
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J.,
 1 (bases 1 to 584)
 TITLE Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source 1..584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HS110591"
 /tissue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
 Pred. No.: 4.21e+03 Length: 584
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP263059 (1-584)

QY 1 SerleulleThrTpAsnIle 7
 DB 266 TCTCTCATTAACCTGGAAATATT 286

RESULT 61
 BP274942
 LOCUS BP274942 Sugano cDNA library, kidney Homo sapiens cDNA clone
 DEFINITION BP274942 Sugano cDNA library, kidney Homo sapiens cDNA clone
 ACCESSION BP274942
 VERSION BP274942.1 GI:52188674
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J.,
 1 (bases 1 to 584)
 TITLE Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source 1..584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SZR01143"
 /tissue_type="brain"
 /clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:
 Pred. No.: 4.21e+03 Length: 584
 Score: 38.00 Matches: 7

AUTHORS Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source 1..584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KDN02414"
 /tissue_type="kidney"
 /clone_lib="Sugano cDNA library, kidney"

ORIGIN

Alignment Scores:
 Pred. No.: 4.21e+03 Length: 584
 Score: 38.00 Matches: 7

QY 1 SerleulleThrTpAsnIle 7
 DB 310 TCTCTCATTAACCTGGAAATATT 330

RESULT 62
 BP348623
 LOCUS BP348623 Sugano cDNA library, brain Homo sapiens cDNA clone
 DEFINITION BP348623 Sugano cDNA library, brain Homo sapiens cDNA clone
 ACCESSION BP348623
 VERSION BP348623.1 GI:52278608
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J.,
 1 (bases 1 to 584)
 TITLE Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source 1..584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SZR01143"
 /tissue_type="brain"
 /clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:
 Pred. No.: 4.21e+03 Length: 584
 Score: 38.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP348623 (1-584)

QY 1 Serleu1eThrTTPAn1le 7
 DB 373 TCTCTCACTTACTCGAATATT 393

RESULT 63 BP236074 588 bp mRNA linear EST 15-SEP-2004
 LOCUS BP236074 Sugano cDNA library, coronary artery endothelial cell Homo
 DEFINITION sapiens cDNA clone HCR06784, mRNA sequence.
 ACCESSION BP236074
 VERSION BP236074.1 GI:52108984
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 588)
 Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
 source
 1..588
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HCR06784"
 /tissue_type="coronary artery"
 /cell_type="endothelial cell"
 /clone_1fb="Sugano cDNA library, coronary artery
 endothelial cell"

ORIGIN
 Alignment Scores:
 Pred. No.: 4.24e+03 Length: 588
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP236074 (1-588)

QY 1 Serleu1eThrTTPAn1le 7
 DB 379 TCTCTCACTTACTCGAATATT 399

RESULT 64 BP348796 588 bp mRNA linear EST 17-SEP-2004
 LOCUS BP348796 Sugano cDNA library, brain Homo sapiens cDNA clone
 DEFINITION SZR01880, mRNA sequence.
 ACCESSION BP348796
 VERSION BP348796.1 GI:52278781
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 588)
 Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
 source
 1..588
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SZR01880"
 /tissue_type="brain"
 /clone_1fb="Sugano cDNA library, brain"

ORIGIN
 Alignment Scores:
 Pred. No.: 4.24e+03 Length: 588
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP348796 (1-588)

QY 1 Serleu1eThrTTPAn1le 7
 DB 370 TCTCTCACTTACTCGAATATT 390

RESULT 65 B1064472 600 bp mRNA linear EST 15-JUN-2001
 LOCUS B1064472 pgfin.pK001.h17 normalised chicken fat cDNA library Gallus gallus
 DEFINITION cDNA clone pgfin.pK001.h17 5', similar to gi17705262
 ref|NF_057678.1| t1xk and tnp receptor-associated protein [Homo
 sapiens] gb|AF64144.1|AF223469_1 (AF223469) AD022 protein [Homo
 sapiens]g, mRNA sequence.
 ACCESSION B1064472
 VERSION B1064472.1 GI:14471994
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauromia; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 600)
 Cogburn,L.A., Morgan,R.W. and Burnside,J.
 TITLE Chicken ESTs from fat
 JOURNAL Unpublished (2001)

COMMENT Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickescr.udel.edu.
 Location/Qualifiers
 1..600
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="pgfin.pK001.h17"
 /sex="Male and Female"
 /tissue_type="fat"
 /lab_host="E. coli EMDH10B"

ORIGIN /clone_11b="normalized chicken fat cdna library"
/note="Vector: pSPORT1"

Alignment Scores:

Pred. No.:	4.35e+03	Length:	600
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B1064472 (1-600)

Qy 1 SerleuileThrTyrpAnile 7
Db 239 TCGTCGATTAACCTGGAATATT 259

RESULT 66
AL703449

LOCUS AL703449 602 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZP686G0621.r1.686 (synonym: h1cc3) Homo sapiens cdna clone
AL703449
ACCESSION AL703449
VERSION AL703449.1 GI:19686804
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Ansoerge,W., Wiltner,U., Mewes,W., Well,B. and Wiemann,S.
TITLE EST (Ansoerge,W., Wiltner,U., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
source 1 (bases 1 to 602)
MIPS

IngoLstraedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZP686G0621) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source 1.602
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686G0621"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_11b="686 (synonym: h1cc3)"
/note="Vector: pTrioPlx2; Site_1: SfiI; Site_2: SfiIb;
CDNA-collection"

ORIGIN

Alignment Scores:

Pred. No.:	4.37e+03	Length:	602
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x AL703449 (1-602)

Qy 1 SerleuileThrTyrpAnile 7
|||||

Db 344 TCTCTCACTTACTGGAATATT 364

RESULT 67

LOCUS AV730762 604 bp mRNA linear EST 17-OCT-2000
DEFINITION AV730762 HTF Homo sapiens cdna clone HTFA010.5', mRNA sequence.
AV730762
ACCESSION AV730762
VERSION AV730762.1 GI:10840183
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Homo sapiens cdna HTF clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source 1.604
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HTFA010"
/issue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_11b="HTF"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	4.38e+03	Length:	604
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x AV730762 (1-604)

Qy 1 SerleuileThrTyrpAnile 7
|||||

Db 385 TCACCTTAACCTGGAATATT 405

RESULT 68

LOCUS CR163431 618 bp DNA linear GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPT insertion targeting and
chromosome engineering clone MPM16824, genomic survey sequence.
CR163431
ACCESSION CR163431
VERSION CR163431.1 GI:49942280
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
1 (bases 1 to 618)
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

Page 34

TITLE
Direct Submission
JOURNAL
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>
FEATURES
source
1. .618
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MMPN168d24"
/clone_1lb="MHPN"

ORIGIN

Alignment Scores:
Pred. No.: 4.5e+03 Length: 618
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR163431 (1-618)

QY
1 SerleuileThrTPanille 7
|||
194 TCATTATTAACCTGGATATTC 174

RESULT 69
CB069952 621 bp mRNA linear EST 21-JAN-2003
LOCUS 18310.Y1 HR85 1stet Homo sapiens cDNA clone IMAGE:6554035 5'
DEFINITION similar to TR:095551 095551 DJ30M3.3 ; mRNA sequence.
ACCESSION CB069952
VERSION CB069952.1 GI:27814472
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 621)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Bresnelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Bilsstein, A.,
Schmitt, A., Treising, B., Rifter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvalli, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 18310.Y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 476.
Location/Qualifiers
1. .621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6554035"
/issue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_1lb="HR85 1stet"

FEATURES

source
1. .621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6554035"
/issue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_1lb="HR85 1stet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Alignment Scores:
Pred. No.: 4.53e+03 Length: 621
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CB069952 (1-621)

QY
1 SerleuileThrTPanille 7
|||
349 TCCTCATTAACCTGGATATTC 369

RESULT 70
BU471395 625 bp mRNA linear EST 30-NOV-2002
LOCUS 603363114F1 CSEQRBN21 Gallus gallus cDNA clone CHEST258K3 5', mRNA
DEFINITION sequence.
ACCESSION BU471395
VERSION BU471395.1 GI:25964972
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 625)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomedical Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1OD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk
Location/Qualifiers
1. .625
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST258K3"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="CSEQRBN21"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methyalted C in the first strand reaction, double-stranded cDNA
was binned, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2

FEATURES

source
1. .625
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST258K3"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="CSEQRBN21"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methyalted C in the first strand reaction, double-stranded cDNA
was binned, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2

ORIGIN rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ALIGNMENT SCORES:

Pred. No.: 4.56e+03 Length: 625
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B0471395 (1-625)

Qy 1 SerLeuileThrTyrPasnile 7
Db 286 TCGCTGATTACTTGGAACATT 306

RESULT 71

LOCUS CB157906 634 bp mRNA linear EST 29-JAN-2003
DEFINITION K-EST0217150 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-5-F06
ACCESSION CB157906
VERSION CB157906.1 GI:28143040
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 634)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

21C Frontier Korean EST Project 2001
Unpublished (2002)

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr

Plate: 5 row: F column: 06
High quality sequence stop: 634.
Location/Qualifiers
1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L18POOL1n1-5-F06"
/cell_line="SNV-354+Cho-CK+Choi-CK+HLK-3"
/lab_host="Top10P"
/clone_11b="L18POOL1n1"
/note="Organ: liver; Vector: pT73-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

FEATURES

source

ORIGIN

ALIGNMENT SCORES:

Pred. No.: 4.64e+03 Length: 634
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CB157906 (1-634)
Qy 1 SerLeuileThrTyrPasnile 7
Db 295 TCTCATTAAGTGGAAATTT 315

RESULT 72

LOCUS CV023369 634 bp mRNA linear EST 20-AUG-2004
DEFINITION 288 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC017553, mRNA sequence.
ACCESSION CV023369
VERSION CV023369.1 GI:51481130
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 634)
Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cho,D., Moore,T.,
Simmons,B., Segueria,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
Vandenhaute,J., Cusick,M.E., Albelia,J.S., Hill,D.E. and Vidal,M.
Human ORFeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers
FORWARD: ATGAGTTGGGAGTTCCTGGA
BACKWARD: TACATATATATCTAGTGCACAGAG
Insert Length: 634 Std Error: 32.00
Plate: 11008 row: 05 column: F
Seq primer: ACTGCCCTCGTTTACACCTCGTACTGGGAAAC
High quality sequence start: 97
High quality sequence stop: 633
POLYA=No.

Location/Qualifiers
1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_11b="Full length cDNA from the Mammalian Gene
Collection"
/note="Vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor vector. Reference : MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"

FEATURES

source

ORIGIN

ALIGNMENT SCORES:

Pred. No.: 4.64e+03 Length: 634
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CV023369 (1-634)

```

y      1 SerLeu11eThrTPaaNtlle 7
|      |
|      |
Db     343 TCTCATTACTGGAAATATT 363

RESULT 73
LOCUS   B1333830
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
1 (bases 1 to 644)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straussberg, Ph.D.
Email: CGapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Pisae: L1AM1348 .cov: n column: 10
High quality sequence scop: 531.
location/Qualifiers
1..644
    /organism="Homo sapiens"
    /mol_type="RNA"
    /db_xref="xref:GeneID:5141577"
    /clone_image="IMAGE:5141577"
    /cvs="cvs:cdna:carcinoma cell line"
    /lab_name="L1AM1348"
    /ad_nos="1"
    /clone_id="NIH_MGC_12"
    /notes="Organ: cervix; vector: pCMV-Sport6; site 1: NoCI;
site 2: Salt; cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN
Alignment Scores:
Pred. No.:          4,73e+03          length:        644
Score:              38.00             Matches:         7
Percent Similarity: 100.0%            Mismatch:       0
Best Local Similarity: 100.0%          Mismatch:       0
Query Match:        100.0%            Gaps:           0
DB:                  3                Gaps:           0

US-10-757-745-2_COPY_115_121 (1-7) x B1333830 (1-644)
QY
1 SerLeu11eThrTPaaNtlle 7
|      |
|      |
Db     330 TCTCATTAAGCTGGAATATT 350

RESULT 74
LOCUS   AZ360347
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

SciUroganathi; Muroidae; Muridae; Murine; Mus.
1 (Bases 1 to 644)
Dunn,D., Aoyagi,A., Barber,M., Bascorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: M column: 01
Seq primer: CACACGAGAAACAGCTATAC
Class: plasmid ends
High quality sequence stop: 644.
Location/Qualifiers
1..644
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0103M01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD22ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD22 (g11473114[BP]A129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Prod. No.: 4.73e+03 Length: 644
Score: 38.00 Matches: 7
Percent Similarity: 100.04 Conservative: 0
Basic local Similarity: 100.04 Mismatches: 0
Query Match: 100.04 Indels: 0
Dbl: 9 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AZ360347 (1-644)

QY 1 Serleu1emhTrrpantlle 7
|||||
62 TCTTTATTAACCTCGAATATC 82

DB

RESUIT. 75 645 bp mRNA linear EST 30-JAN-2002
B426270
LOCUS
DEFINITION
Pgf2n-pK002_c6 Normalized Chicken Abdominal Fat Library (Pgf2n)
calfs skeletal cDNA clone pgf2n-pK002_c6 5' similar to g11418470
ref|Xf_004263.1| TRAF and TNF receptor-associated protein (Homo

sapiens) gi|14747264 ref|XP_041296.1| TRAF and TNF
 receptor-associated protein [Homo sapiens] emb|CAA21141.1|
 (AL031775) dfj30M3.3 (novel protein similar to C. elegans, mRNA
 sequence.
 accession BM426270.1 GI:18430455
 version DKFZp4691195_F1_469 (synonym: Pongo pygmaeus cDNA clone
 sequence.
 source EST
 organism Gallus gallus (chicken)
 keywords Gallus gallus
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 authors 1 (bases 1 to 645)
 title Cogburn, L.A., Morgan, R. and Burnside, J.
 journal ESTs from Normalized Chicken Fat cDNA library- USDA/IRAFs Animal
 genome project
 comment Unpublished (2002)
 journal Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.
 features
 source location/Qualifiers
 1..645
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Commercial broiler, Ottawa Research Centre,
 leghorn"
 /db_xref="taxon:9031"
 /clone="pgfzn.pk002.c6"
 /sex="Male and Female"
 /tissue_type="Abdominal Fat"
 /dev_stage="Embryonic (d18,d19) ; post-hatch
 (d1,w3,w7,w9,w16,1yr)"
 /lab_host="E. coli BMDH10B"
 /clone_lib="Normalized Chicken Abdominal Fat Library
 (pgfzn)"
 /note="Vector: pCMVSPORT6; library made from equivalent
 pools of total RNA isolated from each developmental age
 (across strains); single pass sequencing from 5'-end"
 origin
 Alignment Scores:
 Pred. No.: 4.74e+03 Length: 645
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x BM426270 (1-645)
 Oy 1 SerLeuIleThrTTPaAnIle 7
 Db 373 TCGCTGATACCTTGGAACATT 393
 RESULT 76
 CR753214 652 bp mRNA linear EST 01-SEP-2004
 LOCUS DKFZp4691195_F1_469 (synonym: Pongo pygmaeus cDNA clone
 definition DKFZp4691195_5', mRNA sequence.
 accession CR753214
 version CR753214.1 GI:51845629
 keywords EST.
 source Pongo pygmaeus (orangutan)
 organism Pongo pygmaeus
 keywords Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Pongo.
 reference 1 (bases 1 to 652)
 authors Anorge, W., Krieger, S., Regiert, T., Rittmeyer, C., Schwager, B.,
 Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and

Wiemann, S.
 Pongo pygmaeus mRNA (Anorge, W., Krieger, S., Regiert, T., et al.)
 unpublished (2004)
 comment JOURNAL
 contact: MIPS
 MIPS
 Ingolstaetter Landstr. 1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email: s.wiemann@dkfz-heidelberg.de; lin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp4691195
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
 features
 source location/Qualifiers
 1..652
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp4691195"
 /tissue_type="Kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="469 (synonym: pkid1)"
 /note="Vector: pSPORT1_Sfi; Site_1: SfiI; Site_2: SfiIb"
 origin
 Alignment Scores:
 Pred. No.: 4.8e+03 Length: 652
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x CR753214 (1-652)
 Oy 1 SerLeuIleThrTTPaAnIle 7
 Db 360 TCTTCATACCTGGAATATT 380
 RESULT 77
 CN298920 657 bp mRNA linear EST 16-MAY-2004
 LOCUS CN298920
 definition 1700600170525 GRN_PRENEM Homo sapiens cDNA 5', mRNA sequence.
 accession CN298920
 version CN298920.1 GI:47315334
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens
 keywords Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 reference 1 (bases 1 to 657)
 authors Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murrage, J., Fisk, G.J.,
 Li, Y., Xu, C., Rang, R., Guegler, K., Rao, M.S., Mandel, R.,
 Lebkowksi, J. and Stanton, L.W.
 transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 15146197
 comment Contact: Brandenberger R.
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 insert length: 657 Std Error: 0.00.
 features
 source location/Qualifiers
 1..657
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

ORIGIN

/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_idb="GRN_PRENEMU"
/note="Oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

Alignment Scores:

Pred. No.:	4.84e+03	Length:	657
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CN298920 (1-657)

QY 1 SerleuileThrtTpansnile 7

Db 299 TCTCTACTACTCGAATATT 319

RESULT 78

LOCUS B1067773 662 bp mRNA linear EST 15-JUN-2001
DEFINITION pgfin.pk007.d9 normalized chicken fat cDNA library Gallus gallus

CDNA clone pgfin.pk007.d9 5' similar to gi11418470
ref|XP_004263.1| TRAF and TNF receptor-associated protein [Homo
sapiens] emb|CAA21141.1| (AL031175) dj30M3.3 (novel protein similar
to C. elegans Y63D3A.4) [Homo sapiens] emb|CAB92966.1| (AJ269473)
TRAF and TNF receptor associated prote, mRNA sequence.

ACCESSION

VERSION B1067773.1 GI:14475295

KEYWORDS

SOURCE EST.
ORGANISM Gallus gallus (chicken)
Gallus gallus

REFERENCE

AUTHORS Cogburn,L.A., Morgan,R.W. and Burnside,J.
TITLE Chicken ESTs from fat
JOURNAL Unpublished (2001)
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES

Location/Qualifiers
1..662
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgfin.pk007.d9"
/sex="Male and Female"
/tissue_type="fat"
/lab_host="E.coli EMDH10B"
/clone_idb="normalized chicken fat cDNA library"
/note="Vector: pSPORT1"

ORIGIN

Alignment Scores:

Pred. No.:	4.89e+03	Length:	662
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B1067773 (1-662)

QY 1 SerleuileThrtTpansnile 7

Db 295 TCTCTACTACTCGAATATT 315

RESULT 79

LOCUS B6719113 678 bp mRNA linear EST 08-MAY-2001
DEFINITION 60269045F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831186 5',
mRNA sequence.

ACCESSION B6719113
VERSION B6719113.1 GI:13998300

KEYWORDS

SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: ILAM10753 row: 1 column: 11
High quality sequence stop: 672.
Location/Qualifiers
1..678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4831186"
/lab_host="DH10B"
/clone_idb="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gcgagc); Oligo-dt primed using primer
5'-TTTTTTTTTTTTTAA-3', size-selected for average
insert size 2.2 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

FEATURES

Location/Qualifiers
1..678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4831186"
/lab_host="DH10B"
/clone_idb="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gcgagc); Oligo-dt primed using primer
5'-TTTTTTTTTTTTTAA-3', size-selected for average
insert size 2.2 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	5.03e+03	Length:	678
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B6719113 (1-678)

QY

Db 365 TCTCTACTACTCGAATATT 385

RESULT 80

LOCUS CR767236 701 bp mRNA linear EST 23-SEP-2004
DEFINITION DKFZp469E1236 r1 469 (synonym: pki1) Pongo pygmaeus cDNA clone
DKFZp469E1236 5', mRNA sequence.

ACCESSION

CR767236

VERSION CR767236.1 GI:52609173
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Pongo.
 REFERENCE 1 (bases 1 to 701)
 AUTHORS Ansoerge, W., Krieger, S., Regiert, T., Rittmüller, C., Schwager, B.,
 Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and
 Wiemann, S.
 TITLE Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 JOURNAL Unpublished (2004).
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email: s.wiemann@dkfz-heidelberg.de; flin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469B1236
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
 FEATURES
 source
 1..701
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp469B1236"
 /tissue_type="kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_id="469 (synonym: pklid)"
 /note="Vector: pSPORT1_Sfi; Site_1: SfiIa; Site_2: SfiIb"
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.23e+03 Length: 701
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x CR767236 (1-701)
 Oy 1 SerleuilethrtTpAnlle 7
 |||||
 DB 271 TCTCTCATTACTCGAATATT 291
 RESULT 81
 BI334820 704 bp mRNA linear EST 30-JUL-2001
 LOCUS 60298939F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141193 5',
 DEFINITION mRNA sequence.
 ACCESSION BI334820
 VERSION BI334820.1 GI:15019477
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 704)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LHAM11347 row: n column: 10
 High quality sequence stop: 704.
 FEATURES
 source
 1..704
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5141193"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_id="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.26e+03 Length: 704
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x BI334820 (1-704)
 Oy 1 SerleuilethrtTpAnlle 7
 |||||
 DB 331 TCTCTCATTACTCGAATATT 351
 RESULT 82
 BU661472 710 bp mRNA linear EST 30-SEP-2002
 LOCUS C172d11.21 Hembase; Erythroid Precursor Cells (LCB:c1 library) Homo
 DEFINITION sapiens cDNA clone c172d11 5', mRNA sequence.
 ACCESSION BU661472
 VERSION BU661472.1 GI:23373654
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 710)
 AUTHORS Gubin, A.N., Lee, Y.T., Bouffard, G.G. and Miller, J.L.
 TITLE Gene Expression in Human Erythroid Precursor Cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jwm7@nih.gov
 The 'c1' library was constructed by Alexander Gubin, Ph.D. in the
 Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
 analyses by National Institutes of Health Intramural Sequencing
 Center (NISC). More information available at:
 http://hembase.nidk.nih.gov
 Plate: 72 row: d column: 11
 Seq primer: 5' lambda-TripLex2 Sequencing primer.
 FEATURES
 source
 1..710
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="c172d11"
 /sex="unknown"

ORIGIN

Alignment Scores:

Pred. No.: 5.31e+03 Length: 710
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU61472 (1-710)

QY 1 SerLeu1leThrTPAan1le 7
DB 259 TCTCTCATTAACCTGGAATATT 279

RESULT 83
CN298923 711 bp mRNA linear EST 16-MAY-2004
LOCUS CN298923 17000600002122 GRN_PPREHP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN298923
ACCESSION CN298923
VERSION CN298923.1 GI:47315337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 711)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, W.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 711 Std Error: 0.00.
Location/Qualifiers
1..711
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

FEATURES
source

/tissue_type="blood"
/cell_type="Erythroid Precursor Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Precursor erythroblasts; GPA++"
/lab_host="DH5alpha"
/clone_1lb="Hembase; Erythroid Precursor Cells (LCB:c1
library)"
/note="Organ: blood; Vector: pTriplex2; Site_1: SfiI;
Site_2: SfiI; A complementary DNA (cDNA) library from
human erythroid precursor cells was constructed using
SMART PCR (polymerase chain reaction) cDNA Library
Construction Kit (Clontech, Palo Alto, CA) according to
the manufacturer's directions, but with slight
modifications. Briefly, reverse transcription was
performed in the presence of 1 umol/L peptide nucleic acid
(PNA) oligos
(N-terminal)-biotin-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and
(N-terminal)-biotin-CTT/C-T-GAA-GTT-CTC-AGG-A-(C-terminal)
size-selected on a 1% agarose gel (>800bp). Large-scale
sequencing of the library was performed by the NIH
Intramural Sequencing Center (NISC;
Http://www.nisc.nih.gov/)."

/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_1lb="GRN_PPREHP"
/note="Oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 5.32e+03 Length: 711
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN298923 (1-711)

QY 1 SerLeu1leThrTPAan1le 7
DB 308 TCTCTCATTAACCTGGAATATT 328

RESULT 84
CN500X2P 720 bp DNA linear GSS 28-JUN-1999
LOCUS CN500X2P
DEFINITION Arabidopsis thaliana genome survey sequence SP6 end of BAC T1A24
of T1MU library from strain Columbia of Arabidopsis thaliana,
genomic survey sequence.
ACCESSION AL094351 GI:5295505
VERSION AL094351
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsid.
1 (bases 1 to 720)
Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
Unpublished
2 (bases 1 to 720)
Genoscope.
Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
1..720
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_1lb="T1A24"
/clone_1lb="T1MU"
/ecotype="Columbia"
/note="end : SP6"

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 5.4e+03 Length: 720
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN500X2P (1-720)

QY 1 SerLeu1leThrTPAan1le 7
DB 308 AGTTGATTAACCTGGAACATA 328

RESULT 85
CN298922

LOCUS CN298922 729 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700060007717 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN298922
VERSION CN298922.1 GI:47315336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 729)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
JOURNAL PUBMED
COMMENT Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-created H9 cell
line"
/clone_11b="GRN PREHEP"
/note="oligo dt primed, full-length enriched cDNA library
from DMSO-created hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Alignment Scores:
Pred. No.: 5.48e+03 Length: 729
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CN298922 (1-729)

QY 1 SerLeuIleThTTPasnlle 7
Db 335 TCTCTCATTACCTGGAATATT 355

RESULT 86
LOCUS CN298924 729 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424496911 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN298924
VERSION CN298924.1 GI:47315338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 729)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197

COMMENT Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_11b="GRN ES"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Alignment Scores:
Pred. No.: 5.48e+03 Length: 729
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CN298924 (1-729)

QY 1 SerLeuIleThTTPasnlle 7
Db 277 TCTCTCATTACCTGGAATATT 297

RESULT 87
LOCUS CX760857 731 bp mRNA linear EST 24-JAN-2005
DEFINITION AGENCOURT 40963383 NIH MGC 281 Homo sapiens cDNA clone
IMAGE:77835600 3', mRNA sequence.
ACCESSION CX760857
VERSION CX760857.1 GI:58057513
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 731)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bldg31@mail.nih.gov
Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LHAM15944 row: b column: 14
High quality sequence stop: 574.
Location/Qualifiers
1..731
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_11b="IMAGS:77835600"
/tissue_type="pluripotent cell line derived from

Alignment Scores:

Pred. No.:	Length:	Matches:
5.74e+03	757	38.00
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	100.0%	Indels: 0
DB:	Gaps: 0	

US-10-757-745-2_COPY_115_121 (1-7) x B1760756 (1-757)

QY 1 SerLeu1eThrTPan1le 7

Db 251 TCTCTCATTAAGTGGATATT 271

RESULT 93

LOCUS B1758848

DEFINITION 60286663P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:510303 5',

ACCESSION B1758848.1 GI:14815606

VERSION B1758848.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catearrhini; Homiidae; Homo

REFERENCE NIH-MGC http://mgs.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: gregbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: L14M1264 row: m column: 16

High quality sequence stop: 758.

Location/Qualifiers

1..761

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:510303"

/cdate="IMAGE:510303"

/rname_type="sarvical carcinoma cell line"

/lab_host="DH10B"

/cdate="11b-NIH_MGC_12"

/note="Organ: testis; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed; Average insert size 1.4 kb. Library prepared by Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:

Length:	Matches:
5.83e+03	767
Score:	38.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1258848 (1-767)

QY 1 SerLeu1eThrTPan1le 7

Db 280 TCTCTCATTAAGTGGATATT 300

RESULT 94

LOCUS B6391295

DEFINITION 60241734P1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4536634 5',

ACCESSION B6391295

VERSION B6391295.1 GI:13284743

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catearrhini; Homiidae; Homo

REFERENCE NIH-MGC http://mgs.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: gregbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: L14M10460 row: h column: 11

High quality sequence stop: 693.

Location/Qualifiers

1..770

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4536634"

/rname_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/cdate="11b-NIH_MGC_92"

/note="Organ: testis; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed; Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:

Length:	Matches:
5.85e+03	770
Score:	38.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B6391295 (1-770)

QY 1 SerLeu1eThrTPan1le 7

Db 353 TCTCTCATTAAGTGGATATT 373

RESULT 95

LOCUS B1754101

LOCUS B1754101 774 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603027659F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197838.5',
 mRNA sequence.
 ACCESSION B1754101
 VERSION B1754101.1 GI:15745679
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 774)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11495 row: f column: 15
 High quality sequence stop: 756.
 Location/Qualifiers
 1..774
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5197838"
 /lab_host="DH10B"
 /clone_1ib="NIH_MGC_114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	5.89e+03	Length:	774
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B1754101 (1-774)

QY 1 Serleuilethrtpranlle 7
 |||||
 402 TCTTCATTACTCGAATATT 422

RESULT 96
 B1754579 760 bp mRNA linear EST 27-APR-2004
 LOCUS B1754579
 DEFINITION B1754579 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
 cDNA clone CS0DB007YB11 5-PRIME, mRNA sequence.
 ACCESSION B1754579
 VERSION B1754579.2 GI:46618956
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 780)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 8, 2003 this sequence version replaced gi:30452317.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?e=CS0DB007CA06QP1&c=3474.r.

FEATURES
 source
 1..780
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DB007YB11"
 /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
 /clone_1ib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	5.94e+03	Length:	780
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B1754579 (1-780)

QY 1 Serleuilethrtpranlle 7
 |||||
 DB 355 TCTTCATTACTCGAATATT 375

RESULT 97
 BU406549 782 bp mRNA linear EST 27-NOV-2002
 LOCUS BU406549
 DEFINITION 603483616F1 CSEQCHN59 Gallus gallus cDNA ChESTJ374p3 5', mRNA
 sequence.
 ACCESSION BU406549
 VERSION BU406549.1 GI:25775605
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 782)
 Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 12445392
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..782

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, H1sex"
/db_xref="taxon:9031"
/clone="CHS1374p3"
/dev_stage="36"
/lab_host="DH10B"
/lab_host="CSOCHN59"
/note="Organ: Limbs; Vector: pBluescript II KS(+); Site: 1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:
Pred. No.: 5.96e+03 Length: 782
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 5

US-10-757-745-2_COPY_115_121 (1-7) x BU406549 (1-782)

OY 1 SerLeuLeuThrTPanIle 7

Db 345 TCGCTGATTAAGTGGAAATTT 365

RESULT 98 783 bp mRNA linear EST 08-APR-2004
BX365835
LOCUS BX365835 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens

DEFINITION CDNA clone CS0DB007YB11 5-PRIME, mRNA sequence.
ACCESSION BX365835.2 GI:46288859

VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo

REFERENCE 1 (bases 1 to 783)
AUTHORS Li, W.B., Gruber, C., Tesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT On May 5, 2003 this sequence version replaced gi:30370946.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/csi/DB0022F03QPLKc-3474.r.
Location/Qualifiers
1..783
1..783
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES

source

/clone="CS0DB007YB11"
/rname_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 5.97e+03 Length: 783
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 5

US-10-757-745-2_COPY_115_121 (1-7) x BX365835 (1-783)

OY 1 SerLeuLeuThrTPanIle 7

Db 355 TCGCTGATTAAGTGGAAATTT 375

RESULT 99 786 bp mRNA linear EST 08-MAY-2001
BG719977
LOCUS BG719977 602691335F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4823432 5',
DEFINITION mRNA sequence.
ACCESSION BG719977
VERSION BG719977.1 GI:13999164

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo

REFERENCE 1 (bases 1 to 786)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: CGR@ds-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.jnl.gov
Plate: LHAM0733 row: F column: 09

High quality sequence stop: 784.
Location/Qualifiers
1..786
1..786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4823432"
/lab_host="DH10B"
/clone_lib="NIH MGC 97"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(GTCGAG); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.2 kb and normalized to R05. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC library."

FEATURES

source

ORIGIN
Alignment Scores:

Pred. No.: 6e+03 Length: 786
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BG719977 (1-786)

QY 1 SerleuilethrTPAenile 7
 DB 488 TCTCTCATTAACCTGGACATT 508

RESULT 100
 AJS97426 789 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 DEFINITION 450603, genomic survey sequence.
 ACCESSION AJS97426
 VERSION AJS97426.1 GI:37947054
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chevin, S., Bechold, N., Cnaud, C., Derose, R., Pelletier, G.,
 Lepoint, L., Caboche, M., and Lecharny, A.
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
 PUBMED 12446565
 2 (bases 1 to 789)
 Balzerque, S.
 REFERENCE Direct Substitution
 AUTHORS Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 JOURNAL Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
 http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (http://www.genoplante.com and
 http://genoplante-info.intobiogen.fr).

FEATURES
 source
 1..789
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="450603"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 1..789
 misc_feature
 /note="T-DNA flanking sequence
 left border"

ORIGIN
 Alignment Scores:
 Pred. No.: 6.03e+03 Length: 789
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 10 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AJS97426 (1-789)

QY 1 SerleuilethrTPAenile 7
 DB 223 AGTTGATTACTTGGAACATA 243

RESULT 101
 BG533717 793 bp mRNA linear EST 03-APR-2001
 LOCUS 602562373P1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4700059 5',
 DEFINITION mRNA sequence.
 ACCESSION BG533717
 VERSION BG533717.1 GI:13525257
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LNCM153 row: a column: 20
 High quality sequence stop: 666.

FEATURES
 source
 1..793
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4700059"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 76"
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggcgcttcggcgc); Site 2: SfiI (ggcgcttcggcgc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCCATTAAGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGCGCGCGCATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.85
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC library."

ORIGIN
 Alignment Scores:
 Pred. No.: 6.06e+03 Length: 793
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BG533717 (1-793)

QY 1 SerleuilethrTPAenile 7
 DB 198 TCTCTCATTAACCTGGAAATAT 218

RESULT 102
 CX756424 799 bp mRNA linear EST 24-JAN-2005
 LOCUS AGENCOURT_41337854 NIH_MGC_281 Homo sapiens cDNA clone
 DEFINITION IMAGE:779791 3', mRNA sequence.
 ACCESSION CX756424
 VERSION CX756424.1 GI:58053080

KEYWORDS	Est. sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homininae (to 799)
REFERENCE	NIH-MGC http://mhc.ncbi.nlm.nih.gov/
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	
COMMENT	Contact: Daniela S. Gehrad, Ph.D.

FEATURES	Location/Qualifiers
source	1. .799

Alignment Scores:

Pred. No.:	6.12e+03	Length:	799
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Incls:	0
DB:	8	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) X CX756424 (1-799)

QY 1 SerLeuileThrTyrPasnile 7
|||
Db 360 TCCTCATTAAGTGAATATT 380

RESULT 103	
CX166335	810 bp mRNA linear EST 23-DEC-2004
LOCUS	
DEFINITION	HSSCC_39 B09.G1 A035 NIH MG-C 258 Homo sapiens CDNA clone
IMAGE:7469923 5', mRNA sequence.	
ACCESSION	
CX166335	
VERSION	
CX166335.1	GI:56796415
KEYWORDS	EST.

SOURCE ORGANISM	Source
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
Hominae; Homo.	
1 (bases 1 to 810)	
NIH-MGC http://mgc.nci.nih.gov/ .	
National Institutes of Health, Mammalian Gene Collection (MGC)	
Unpublished (1999)	
Contact: Daniela S. Gerhard, Ph.D.	
JOURNAL COMMENT	

FEATURES

Location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.:	6.22e+03	Length:	870
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) X CX166335 (1-810)

```
QY      1 Serleuiietrrtipasnile ?  
         |||||  
Db     300 TCTCTCATTACCTGGAATATT 320
```

RESULT 104	817 bp	mRNA	linear	EST 25-NOV-2002
BUI11103				
LOCUS				
BUI11103				

DEFINITION 603127011F1 CSECHL13 Gallus gallus cDNA clone CHEST97f3 5', mRNA sequence.

ACCESSION BU111103

VERSION BU111103.1 GI:25314803

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken CDNA

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

PUBMED 12445392

COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1..817, Location/Qualifiers

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, Hisex"

/db_xref="taxon:9031"

/clone="CHEST97f3"

/dev_stage="22"

/lab_host="DH10B"

/clone_11b="CSECHL13"

/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)-Trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. ligate in double stranded adaptor containing BspI and BamH sites [5'ggcgcgcgcagcccgatccgaaataag] [5'aattcttttcggtatccg99g9cgcgcg]"

ORIGIN

Alignment Scores:

Pred. No.:	6.28e+03	Length:	817
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU111103 (1-817)

QY 1 SerLeuIleThrTrpAsnIle 7

DB 378 TCGCTGATTAACCTTGGAAACATT 398

RESULT 105

CZ953332 818 bp DNA linear GSS 11-AUG-2005

LOCUS 265164 Tomato EcoRI BAC library Lycopersicon esculentum genomic

DEFINITION clone SL_ECOR10056K18 5, genomic survey sequence.

ACCESSION CZ953332

VERSION CZ953332.1 GI:72298562

KEYWORDS GSS.

SOURCE Lycopersicon esculentum (Solanum lycopersicum)

ORGANISM Lycopersicon esculentum

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 818)

AUTHORS Mueller, L.A., Buel, R.M., Wang, Y., Tankley, S.D., Giovannoni, J.J., Van Eck, J. and Stack, S.

TITLE BAC end sequencing from three Solanum lycopersicon libraries

JOURNAL Unpublished (2005)

COMMENT Other_GSSs: 269931

Contact: Lukas Mueller

Tanksley Lab, Dept. of Plant Breeding

Cornell University

251 Emerson Hall, Ithaca, NY 14853, USA

Tel: 607-255-6557

Fax: 607-255-6683

Email: sgn-feedback@cornell.edu

Plate: 56 row: K column: 18

Seq primer: 77

Class: BAC ends

High quality sequence stop: 579.

FEATURES

source

1..818 Location/Qualifiers

/organism="Lycopersicon esculentum"

/mol_type="genomic DNA"

/cultivar="Heinz 1706"

/db_xref="taxon:4081"

/clone="SL_ECOR10056K18"

/lab_host="E. coli"

/clone_11b="Tomato EcoRI BAC library"

/note="Vector: unk; Site 1: EcoRI"

ORIGIN

Alignment Scores:

Pred. No.:	6.29e+03	Length:	818
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CZ953332 (1-818)

QY 1 SerLeuIleThrTrpAsnIle 7

DB 622 AGCTTTTAACTTGGAAACATT 642

RESULT 106

B1908925 838 bp mRNA linear EST 16-OCT-2001

LOCUS 603067028F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215926 5',

DEFINITION mRNA sequence.

ACCESSION B1908925

VERSION B1908925.1 GI:16172029

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 838)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLML1542 row: h column: 07

High quality sequence stop: 773.

FEATURES

source

1..838 Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="IMAGE:5215926"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_id="NIH_MGC_118"
/note="Vector: PCMV-SPOK6, Site_1: NotI, Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (SPOK6 site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 027. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 6.48e+03 Length: 838
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1908925 (1-838)

OY 1 SerLeu1eThrTPaen1le 7

DB 344 TCTCTCATTAAGTGAATATT 364

RESULT 107
LOCUS CR765451 846 bp mRNA linear EST 23-SEP-2004
DEFINITION DKFZP469E2434.1 469 (synonym: PK1d1) Pongo pygmaeus cDNA clone
ACCESSION CR765451
VERSION CR765451.1 GI:5260526
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Pongo.
1 (bases 1 to 846)
Ostenwelder, B.; Obermaier, B.; Deutschenbaur, S.; Schaipp, A.;
Mewes, H.W.; Weil, B.; Amlid, C.; Oesinger, A.; Fobo, G.; Han, M. and
Wiemann, S.

REFERENCE
AUTHORS

TITLE Pongo pygmaeus mRNA (Ostenwelder, B., Obermaier, B.,
Deutschenbaur, S., et al.)
JOURNAL Unpublished (2004)
COMMENT MIPS

FEATURES
source
1..846
Location/Qualifiers
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone_id="DKFZP469E2434"
/tissue_type="kidney"
/dev_stage="adult"

/lab_host="DH10B"
/clone_id="469 (synonym: PK1d1)"
/note="Vector: pSPORT1_SfiI, Site_1: SfiIA, Site_2: SfiIB"

ORIGIN

Alignment Scores:
Pred. No.: 6.55e+03 Length: 846
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR765451 (1-846)

OY

DB 246 TCTCTCATTAAGTGAATATT 266

RESULT 108
LOCUS BE784416 853 bp mRNA linear EST 20-OCT-2000
DEFINITION 601473891F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876862 5',
RNA sequence.
ACCESSION BE784416
VERSION BE784416.1 GI:10205614
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 853)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DRP/Gasdar
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM638 row: e column: 23
High quality sequence stop: 660.
Location/Qualifiers

FEATURES
source

1..853
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="IMAGE:3876862"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_68"
/note="Organ: Lung; Vector: PCMV-SPOK6, Site_1: NotI,
Site_2: SfiI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 6.61e+03 Length: 853
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BE784416 (1-853)

OY 1 SerLeu1eThrTPaen1le 7

Db 347 TCTCATTAACCTGGAAATTT 367

RESULT 109
BI553412 858 bp mRNA linear EST 05-SEP-2001
LOCUS 603193558F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5264582 5',
DEFINITION
ACCESSION BI553412
VERSION BI553412 GI:15440724
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 858)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1667 row: c column: 15
High quality sequence stop: 829.
Location/Qualifiers
1. 858
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5264582"
/issue_type="hippocampus"
/lab_host="DH10B"
/clone_1ib="NIH_MGC_95"
/note="Organ: Brain; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI, Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTCTTTT-3', size-selected for average
insert size 2.5 kb and normalized to RGT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	6 66e+03	Length:	858
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BI553412 (1-858)

OY 1 SerLeuileThrTyrPasnle 7
|||||
Db 363 TCTCATTAACCTGGAAATTT 383

RESULT 110
BG740396 870 bp mRNA linear EST 15-MAY-2001
LOCUS 602634171F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:479449 5',
DEFINITION
ACCESSION BG740396
MRNA sequence.

VERSION BG740396.1 GI:14051049
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 870)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10636 row: m column: 18
High quality sequence stop: 826.
Location/Qualifiers
1. 870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:479449"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NCI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.:	6 77e+03	Length:	870
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG740396 (1-870)

OY 1 SerLeuileThrTyrPasnle 7
|||||
Db 254 TCTCATTAACCTGGAAATTT 274

RESULT 111
BU159911 870 bp mRNA linear EST 04-SEP-2002
LOCUS AGENCOURT_7933863 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6144208
DEFINITION
ACCESSION BU159911
VERSION BU159911 GI:22673821
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 870)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LHAM13468 row: n column: 17
High quality sequence stop: 677.
Location/Qualifiers

FEATURES

source

1..870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6144208"
/issue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	6.77e+03	Length:	870
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU159911 (1-870)

Qy 1 SerleuileThrTyraenile 7

Db 278 TCTCATTAACCTGGAATATT 298

RESULT 112

LOCUS

BU169945 883 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7913097 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:6024760

DEFINITION

5', mRNA sequence.

ACCESSION

BU169945

VERSION

BU169945.1 GI:22683929

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 883)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LHAM13235 row: m column: 17
High quality sequence stop: 413.
Location/Qualifiers

FEATURES

source

1..883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6024760"
/issue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN

Average insert size 1.8 kb. Library constructed by Life Technologies."

Alignment Scores:

Pred. No.:	6.89e+03	Length:	883
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU169945 (1-883)

Qy

1 SerleuileThrTyraenile 7

Db 223 TCTCATTAACCTGGAATATT 243

RESULT 113

LOCUS

BU179107 883 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7984768 NIH_MGC_71 Homo sapiens CDNA clone IMAGE:6174938

DEFINITION

5', mRNA sequence.

ACCESSION

BU179107

VERSION

BU179107.1 GI:22693091

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 883)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LHAM13548 row: o column: 23
High quality sequence stop: 672.
Location/Qualifiers

FEATURES

source

1..883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6174938"
/issue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."

ORIGIN

Alignment Scores:

Pred. No.:	6.89e+03	Length:	883
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU179107 (1-883)

Qy

1 SerleuileThrTyraenile 7

Db 201 TCTCATTAACCTGGAATATT 221

RESULT 114
LOCUS BG537046 889 bp mRNA linear EST 03-APR-2001
DEFINITION 602565130P1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4689919 5',
RNA sequence.
ACCESSION BG537046
VERSION BG537046.1 GI:13528594
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM1506 row: k column: 08
High quality sequence stop: 525.
Location/Qualifiers
1..889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4689919"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
5'fl (ggcgccgcgcgc); Site_2: 5'fl (ggcgccatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATATGACC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCGACATG-dt(30)NN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 6.95e+03 Length: 889
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 2
US-10-757-745-2_COPY_115_121 (1-7) x BG537046 (1-889)
Qy 1 Serleuilethrtprasnle 7
Db 358 TCTCTCAATTAAGTATTT 378
FEATURES
source
1..889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4689919"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech);
Site_1: 5'fl (ggcgccgcgcgc); Site_2: 5'fl
(ggcgccatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3'

ACCESSION CR212336 889 bp DNA linear GSS 06-JUL-2004
LOCUS CR212336/c
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone WHPN238m07, genomic survey sequence.
ACCESSION CR212336
VERSION CR212336.1 GI:49991185
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 889)
ADAMS D.J., BIGGS P.J., COX A.V., DAVIES R.M., VAN DER WEYDEN L.,
JONKERS J., SMITH J., PLUMB R.W., TAYLOR R.G., NISHIJIMA I., YU Y.,
ROGERS J. and BRADLEY A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>
FEATURES
source
1..889
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="WHPN238m07"
/clone_1lb="WHPN"
Location/Qualifiers
1..889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4770389"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH_MGC_79"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site_1: 5'fl (ggcgccgcgcgc); Site_2: 5'fl
(ggcgccatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3'

ORIGIN
Alignment Scores:
Pred. No.: 6.95e+03 Length: 889
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 11
US-10-757-745-2_COPY_115_121 (1-7) x CR212336 (1-889)
Qy 1 Serleuilethrtprasnle 7
Db 176 TCATTAATTAAGTATTC 156
FEATURES
source
1..889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4770389"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH_MGC_79"
/note="Organ: lung; Vector: pDNR-LIB (Clontech);
Site_1: 5'fl (ggcgccgcgcgc); Site_2: 5'fl
(ggcgccatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3'

ACCESSION BG623866 898 bp mRNA linear EST 18-APR-2001
LOCUS BG623866
DEFINITION 602649018P1 NIH_MGC_79 Homo sapiens CDNA clone IMAGE:4770389 5',
RNA sequence.
ACCESSION BG623866
VERSION BG623866.1 GI:13675237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 898)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM1637 row: d column: 06
High quality sequence stop: 688.
Location/Qualifiers
1..898
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4770389"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH_MGC_79"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site_1: 5'fl (ggcgccgcgcgc); Site_2: 5'fl
(ggcgccatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3'

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ORIGIN

and 3' adaptor sequence:
5'-ATTCTAGGCGCCGAGCGCCGACGACG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC library."

Alignment Scores:

Pred. No.:	7.03e+03	Length:	898
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG623866 (1-898)

OY 1 Serleu1eThrTTPanille 7

DB 530 TCTCTCATTTACTGGAAATAT 550

RESULT 117

BK422491

LOCUS BK422491 Homo sapiens FETAL LIVER Homo sapiens cDNA clone

DEFINITION

CSGDM007YE11 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with NotI and cloned

into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?c=CSGDM007AC06Q1&c=3474.r.

Location/Qualifiers

1..904

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSGDM007YE11"

/tissue_type="FETAL LIVER"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL LIVER"

/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched double-strand cDNA was digested with NotI and

cloned into the NotI and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.:	7.09e+03	Length:	904
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BK422491 (1-904)

OY 1 Serleu1eThrTTPanille 7

DB 286 TCTCTCATTTACTGGAAATAT 306

RESULT 118

LOCUS CD251503

AGENCOURT 14212105 NIH_MGC_179 Homo sapiens cDNA clone

IMAGE:30385385 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with NotI and cloned

into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?c=CSGDM007AC06Q1&c=3474.r.

Location/Qualifiers

1..906

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAG3:30385385"

/tissue_type="Pituitary"

/lab_host="DH10B-Tom A" T1 and T5 phage resistances)

/clone_lib="NIH_MGC_179"

/note="Organ: brain; Vector: pCMV-SPORT6.1; Site: 1; EcoRV

(destroyed); Site: 2; NotI; Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.1 kb. Library was

constructed by (Invitrogen). Note: this is a NIH_MGC

Library."

Location/Qualifiers

1..906

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAG3:30385385"

/tissue_type="Pituitary"

/lab_host="DH10B-Tom A" T1 and T5 phage resistances)

/clone_lib="NIH_MGC_179"

/note="Organ: brain; Vector: pCMV-SPORT6.1; Site: 1; EcoRV

(destroyed); Site: 2; NotI; Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.1 kb. Library was

constructed by (Invitrogen). Note: this is a NIH_MGC

Library."

Location/Qualifiers

1..906

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAG3:30385385"

/tissue_type="Pituitary"

/lab_host="DH10B-Tom A" T1 and T5 phage resistances)

/clone_lib="NIH_MGC_179"

/note="Organ: brain; Vector: pCMV-SPORT6.1; Site: 1; EcoRV

(destroyed); Site: 2; NotI; Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.1 kb. Library was

Page 54

BG391213
LOCUS BG391213 908 bp mRNA linear EST 12-MAR-2001
DEFINITION 602417244F1 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:4536635 5',
RNA sequence.
ACCESSION BG391213
VERSION BG391213.1 GI:13284661
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 908)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10460 row: h column: 12
High quality sequence stop: 732.
Location/Qualifiers
1..908
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4536635"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ALIGNMENT Scores:
Pred. No.: 7.13e+03 Length: 908
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BG391213 (1-908)

QY 1 SerLeuileThrTPAsnIle 7
|||||
Db 346 TCTCTCATTACCTGGAATATT 366

RESULT 120
BI915865 915 bp mRNA linear EST 16-OCT-2001
LOCUS BI915865
DEFINITION 603184522F1 NIH_MGC_121 Homo sapiens CDNA clone IMAGE:55248495 5',
mRNA sequence.
ACCESSION BI915865
VERSION BI915865.1 GI:16179808
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 915)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11627 row: e column: 08
High quality sequence stop: 696.
Location/Qualifiers
1..915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5248495"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ALIGNMENT Scores:
Pred. No.: 7.19e+03 Length: 915
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BI915865 (1-915)

QY 1 SerLeuileThrTPAsnIle 7
|||||
Db 350 TCTCTCATTACCTGGAATATT 370

RESULT 121
BG119064 927 bp mRNA linear EST 30-JAN-2001
LOCUS BG119064
DEFINITION 602347589F1 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:4442399 5',
mRNA sequence.
ACCESSION BG119064
VERSION BG119064.1 GI:12612570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 927)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10215 row: a column: 24

High quality sequence stop: 676.
Location/Qualifiers

FEATURES
Source

1. :327
/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone_image="442399"
/clone_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH-MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1; Note: Site 2: SalI, cloned unidirectionally, oligo-dT primed. Average insert size 1.7 kb library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	7.3e+03	Length:	927
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG119064 (1-927)

QY 1 SerleuileThrTyrPasnile 7
DB 175 TCTCTATTACCTGGATATT 195

RESULT 122

LOCUS BG740339 937 bp mRNA linear EST 15-MAY-2001
DEFINITION 602635289F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4780318 5',
RNA sequence.
ACCESSION BG740339
VERSION BG740339.1 GI:14050992
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homnidae; Homo

REFERENCE 1 (bases 1 to 932)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: James M. Leaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL). DNA
Sequencing by: InCyte Genomics, Inc.
Clone Distribution: MGC clones distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1639 row: a column: 23
High quality sequence stop: 759.
Location/Qualifiers

1. 932
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="4780318"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; Note: Site 2: SstI, cloned unidirectionally, primer: oligo-dT. Average insert size 1.5kb library constructed by Life Technologies. Note: this is a NCI CGAP library."

ORIGIN

Alignment Scores:

Pred. No.:	7.35e+03	Length:	932
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG740339 (1-932)

QY 1 SerleuileThrTyrPasnile 7
DB 174 TCTCTATTACCTGGATATT 194

RESULT 123

LOCUS BG541819 937 bp mRNA linear EST 03-APR-2001
DEFINITION 602569712F1 NIH-MGC_77 Homo sapiens cDNA clone IMAGE:4694066 5',
mRNA sequence.
ACCESSION BG541819
VERSION BG541819.1 GI:13534052
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homnidae; Homo

REFERENCE 1 (bases 1 to 937)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLOUTBCH Laboratories, Inc.
CDNA Library Preparation: CLOUTBCH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: InCyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1517 row: h column: 03
High quality sequence stop: 714.
Location/Qualifiers

1. 937
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="4694066"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH-MGC 77"
/note="Organ: lung; Vector: pBMR-LIB (Clontech); Site: 1; Site 2: SfiI (ggccatcggcc); Site 3: SfiI (ggccatcggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGACATTATGCGC-3' and 3' adaptor sequence: 5'-ATTCTGAGCGCGACGCGCGATGATG-dt(30)-BN-3' (where B = A, C, G, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC library."

FEATURES

Source

ORIGIN

Alignment Scores:

Pred. No.:	7.4e+03	Length:	937
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG541819 (1-937)

QY 1 SerleuileThrTyrPasnile 7

DB 359 TCTCTCATTAAGCTGGAAATATT 379

RESULT 124
BX358707 942 bp mRNA linear EST 08-APR-2004
LOCUS BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1042YL19 5'-PRIME, mRNA sequence.
ACCESSION BX358707.2 GI:46306560
VERSION BX358707.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 942)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30378261.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdnas=CS0D1042CPI00P1ec=3474.r.

FEATURES
source
1..942
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1042YL19"
/library="PLACENTA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched; double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
7.44e+03	38.00	942	7	0	0	0	0
Percent Similarity:	100.0%						
Best Local Similarity:	100.0%						
Query Match:	100.0%						

US-10-757-745-2_COPY_115_121 (1-7) x BX358707 (1-942)

QY 1 SerLeuIIeThTPaSnIle 7

DB 212 TCTCTCATTAAGCTGGAAATATT 232

RESULT 125
BU468774 946 bp mRNA linear EST 30-NOV-2002
LOCUS BU468774 946 bp mRNA linear EST 30-NOV-2002
DEFINITION 60337165F1 CSEQRBN20 Gallus gallus cDNA clone CHEST279b17 5', mRNA
sequence.
ACCESSION BU468774.1 GI:25962351
VERSION BU468774.1
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE
1 (bases 1 to 946)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..946
Location/Qualifiers

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST279b17"
/sex="Male and female"
/library="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched; double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
7.48e+03	38.00	946	7	0	0	0	0
Percent Similarity:	100.0%						
Best Local Similarity:	100.0%						
Query Match:	100.0%						

US-10-757-745-2_COPY_115_121 (1-7) x BU468774 (1-946)

QY 1 SerLeuIIeThTPaSnIle 7

DB 234 TCGCTGATTAAGCTGGAAATATT 254

RESULT 126
CR113807 946 bp DNA linear GSS 05-JUN-2004
LOCUS CR113807 946 bp DNA linear GSS 05-JUN-2004
DEFINITION Forward strand read from insert in 5'HPT insertion targeting and
chromosome engineering clone WHP215K05, genomic survey sequence.
ACCESSION CR113807.1 GI:49861238
VERSION CR113807.1
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Muridae; Mus.
1 (bases 1 to 946)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

Page 58

Jongers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Dissect Submission
TITLE
JOURNAL
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>
FEATURES
SOURCE
1
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN215X05"
/clone_11b="MHPN"

ORIGIN

Alignment Scores:

Pred. No.:	7.48e+03	Length:	946
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CR113807 (1-946)

OY 1 SerLeu1leThrTyrPAsn1le 7

DB 200 TCATTATTAACCTGGATATTC 180

RESULT 127
LOCUS
AL555333
DEFINITION
AL555333 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK007YK05 5-PRIME, mRNA sequence.
ACCESSION
AL555333.3 GI:45860070
VERSION
EST
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 946)
La W.B., Gruber, C., Jessup, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 15, 2001 this sequence version replaced gi:31277141.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DK007AF03QP1&c=3474.r>.

FEATURES
source
1
location/Qualifiers
948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK05"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_11b="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7.5e+03 Length: 948
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x AL555333 (1-946)

ORIGIN

Alignment Scores:

Pred. No.:	7.5e+03	Length:	948
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x AL555333 (1-946)

OY 1 SerLeu1leThrTyrPAsn1le 7

DB 362 TCCTCATTAACCTGGATATTC 382

RESULT 128
LOCUS
BX433489/c
DEFINITION
BX433489 Homo sapiens ADULT BRAIN Homo sapiens CDNA clone
CS0DN005YN02 3-PRIME, mRNA sequence.
ACCESSION
BX433489
VERSION
BX433489.2 GI:47002503
KEYWORDS
EST.
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 952)
La W.B., Gruber, C., Jessup, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On May 15, 2003 this sequence version replaced gi:30775195.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by life technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0BA1056XD12_CS05372_1&c=3474.r.

FEATURES
source
1
location/Qualifiers
952
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN005YN02"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_11b="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

OY 1 SerLeu1leThrTyrPAsn1le 7
|||||

Db 801 TCTCTCATTACCTGGAATATT 781

RESULT 129

LOCUS B1161201 959 bp mRNA linear EST 05-JUL-2001

DEFINITION 602865659F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019639 5',

ACCESSION B1161201

VERSION B1161201.1 GI:14621202

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1CM1835 row: e column: 16
High quality sequence scop: 551.

FEATURES

source

1..959

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5019639"

/tissue_type="epitheloid carcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." |"

ORIGIN

Alignment Scores:

Pred. No.: 7.61e+03 Length: 959

Score: 38.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1161201 (1-959)

Qy 1 SerLeuIIeThrTyrPasnIle 7

Db 361 TCTCTCATTACCTGGAATATT 381

RESULT 130

LOCUS BM468826 972 bp mRNA linear EST 05-FEB-2002

DEFINITION AGENCOURT 6445782 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587154

ACCESSION BM468826

VERSION BM468826.1 GI:18517868

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1LM12356 row: d column: 03
High quality sequence scop: 707.

FEATURES

source

1..972

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5587154"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: testis; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." |"

ORIGIN

Alignment Scores:

Pred. No.: 7.73e+03 Length: 972

Score: 38.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BM468826 (1-972)

Qy 1 SerLeuIIeThrTyrPasnIle 7

Db 238 TCTCTCATTACCTGGAATATT 258

RESULT 131

LOCUS BX338160 981 bp mRNA linear EST 08-APR-2004

DEFINITION BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS001096YC3 5-PRIME, mRNA sequence.

ACCESSION BX338160

VERSION BX338160.2 GI:46283046

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

JOURNAL Full-length cDNA libraries and normalization

COMMENT Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30345671.
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?cs=CSOD1056AB12QPI&c=3474.r>.

FEATURES

source

1. .981
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1056YC23"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	7.81e+03	Length:	981
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BX338160 (1-981)

OY 1 Serleullethrtypasnlle 7

Db 356 TCTCTGATTAAGTGAATATT 376

RESULT 132

LOCUS

CC216952 992 bp DNA linear GSS 12-MAY-2003

DEFINITION

CH261-110N21.RM1.1 CH261 Gallus gallus genomic clone CH261-110N21.

ACCESSION

CC216952

VERSION

CC216952.1 GI:30536676

KEYWORDS

GSS

SOURCE

Gallus gallus (chicken)

ORGANISM

Gallus gallus

REFERENCE

Bukaryova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

AUTHORS

Krentzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

TITLE

Gallus gallus BAC End Reads

JOURNAL

Unpublished (2003)

COMMENT

Contact: Richard K. Wilson

FEATURES

source

High quality sequence start: 25
High quality sequence stop: 786.
Location/Qualifiers
1..992
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-110N21"
/sex="female"
/cell_line="UCD001, inbred 256"
/clone_1ib="CH261"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CH261 Female Chicken library - For library and clone

Ordering information: <http://www.chori.org/bacpac>

ORIGIN

Alignment Scores:

Pred. No.:	7.92e+03	Length:	992
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CC216952 (1-992)

OY 1 Serleullethrtypasnlle 7

Db 423 TCTGATTAAGTGAATATT 443

RESULT 133

LOCUS

BE892886 995 bp mRNA linear EST 20-OCT-2000

DEFINITION

601435730F1 NIH-MGC-72 Homo sapiens cDNA clone IMAGE:3920790.5'

ACCESSION

BE892886

VERSION

BE892886.1 GI:10353510

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

1 (bases 1 to 995)

TITLE

NIH-MGC <http://mgs.nci.nih.gov/>.

JOURNAL

National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

Unpublished (1999)

CONTACT

Contact: Robert Strassberg, Ph.D.

FEATURES

source

High quality sequence start: 573.
High quality sequence stop: 573.
Location/Qualifiers
1..995
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3920790"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH-MGC-72"
/note="Organ: skin; Vector: pCMV-SPORT6, Site 1: NotI, Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	7.95e+03	Length:	995
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BE892886 (1-995)

OY 1 Serleullethrtypasnlle 7

Db 372 TCTGATTAAGTGAATATT 392

RESULT 134
 BX337141 1018 bp mRNA linear EST 07-APR-2004
 LOCUS BX337141 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1036YJ02 5-PRIME, mRNA sequence.
 ACCESSION BX337141
 VERSION BX337141.2 GI:46271144
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 1018)
 L1.W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30337585.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0D1036DE01QPlc=3474.r.

FEATURES
 source
 1..1018
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1036YJ02"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Alignment Scores:
 Pred. No.: 8.17e+03 Length: 1018
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BX337141 (1-1018)

QY 1 SerLeulleThrTPAsnIle 7
 |||||
 Db 333 TCTCTCATTAACCTGGAATAT 353

RESULT 135
 BU235217 1030 bp mRNA linear EST 26-NOV-2002
 LOCUS BU235217 603791177P1 GSEQCEN24 Gallus gallus cDNA clone CHEST754J19 5', mRNA
 DEFINITION sequence.
 ACCESSION BU235217
 VERSION BU235217.1 GI:25480405
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1030)

AUTHORS
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
 1..1030
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST754J19"
 /dev_stage="22"
 /lab_host="DH10B"
 /clone_lib="GSEQCEN24"
 /note="Organ: heads; Vector: pluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was bluntend, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN
 Alignment Scores:
 Pred. No.: 8.28e+03 Length: 1030
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU235217 (1-1030)

QY 1 SerLeulleThrTPAsnIle 7
 |||||
 Db 13 TCGCTGATTAACCTGGAACATT 33

RESULT 136
 BM554324 1035 bp mRNA linear EST 20-FEB-2002
 LOCUS BM554324 AGENCOURT_6546794 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742466
 DEFINITION 5', mRNA sequence.
 ACCESSION BM554324
 VERSION BM554324.1 GI:18793827
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 1035)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bri-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
 Plate: LLM12760 row: K column: 11
 High quality sequence stop: 738.
 Location/Qualifiers

FEATURES

1..1035
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742466"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	8.33e+03	Length:	1035
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BM554324 (1-1035)

QY 1 SerLeuLeTThTTPanille 7
 |||||
 515 TCTCTCATTAACCTGGAATATT 535

RESULT 137

BM926092

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM926092 1046 bp mRNA linear EST 12-MAR-2002
 AGENCOURT 6649780 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5764440
 5' mRNA sequence.
 BM926092.1 GI:19376471
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 1046)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: gsapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
 Plate: LLM12817 row: O column: 01
 High quality sequence start: 4
 High quality sequence stop: 632.
 Location/Qualifiers
 1..1046

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5764440"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.3 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

ORIGIN

Pred. No.:	8.43e+03	Length:	1046
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BM926092 (1-1046)

QY 1 SerLeuLeTThTTPanille 7
 |||||
 216 TCTCTCATTAACCTGGAATATT 236

RESULT 138

EX337905

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EX337905 1067 bp mRNA linear EST 07-APR-2004
 EX337905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1052YN13 5-PRIME, mRNA sequence.
 EX337905
 EX337905.2 GI:46273926
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 1067)
 L.W.B., Gruber, C., Jessee, J., and Polyes, D.
 Full-length cDNA libraries and normalization
 On May 2, 2003 this sequence version replaced gi:30339657.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna/CS0D1052C007QPlac=3474.r>.
 Location/Qualifiers
 1..1067
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1052YN13"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	8.64e+03	Length:	1067
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BX337905 (1-1067)

Qy 1 SerleulleThrTpAsnIle 7

Db 367 TCTCTCATTAACCTGGAAATATT 387

RESULT 139

LOCUS BUI31072 1077 bp mRNA linear EST 25-NOV-2002
 DEFINITION 603116142F1 CSEQCHL21 Gallus gallus cDNA clone CHEST70012 5', mRNA
 sequence.

ACCESSION BUI31072

VERSION BUI31072.1 GI:25343002

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 1077)

Boardman, P.E., Sanz-Bzquez, J., Overton, I.M., Burt, D.W., Bosch, E.,

Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

PIRME

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

FEATURES

source

1..1077

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, Hisex"

/db_xref="taxon:9031"

/clone="CHEST70012"

/dev_stage="36"

/lab_host="DH10B"

/clone_11b="CSEQCHL21"

/note="Organ: trunks; Vector: pBluescript II KS(+);
 Site 1: EcoRI; Site 2: NotI; Modification of pBluescript
 II KS(+) [Stratagene] vector to accommodate cDNA produced
 with the T-timed protocol (Construction of
 uni-directionally cloned cDNA libraries from messenger RNA
 for improved 3' end DNA sequencing by Glenn Fu, et al.
 U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
 NotI and EcoRI. Ligate in double stranded adaptor
 containing BglI and BamHI sites
 [5'ggcgcgcgcgcgcgcgcgcgcgcgaataaag]
 [5'aattcttttctcgatccg99gcgcgcgc]"

US-10-757-745-2_COPY_115_121 (1-7) x BUI31072 (1-1077)

Qy 1 SerleulleThrTpAsnIle 7

Db 358 TCGCTGATTAACCTGGAAATATT 378

RESULT 140

LOCUS BX444691 1081 bp mRNA linear EST 04-MAY-2004
 DEFINITION BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 CS0DN005YN02 5-PRIME, mRNA sequence.

ACCESSION BX444691

VERSION BX444691.2 GI:47009162

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 1081)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30780264.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Creteil, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 3474.r

For more information about this cluster see

http://www.genoscope.cns.fr/cdna?b=CS0DN005DG01QPlc=3474.r.

Location/Qualifiers

FEATURES

source

1..1081

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DN005YN02"

/tissue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_11b="Homo sapiens ADULT BRAIN"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

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VERSION DQ049205.1 GI:66902404
KEYWORDS GSS. sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo
REFERENCE
  1 (bases 1 to 1089)
  Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
  White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
  Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
  Rockville, MD 20850, USA
  A Scan for positively selected genes in the Genomes of Humans and
  Chimpanzees
  (et) PLOS Biol. 3 (6), E170 (2005)
JOURNAL
  15869325
REFERENCE
  1 (bases 1 to 1089)
  Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
  Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
  White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
  Direct Submision
  Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
  Rockville, MD 20850, USA
  This sequence was made by sequencing genomic exons and ordering
  them based on alignment. Translation starts at the beginning of
  alignment.
FEATURES
  source
    1..1089
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="6"
    <1..1089
    /gene="TTRAP"
    /locus_tag="HC17203"
ORIGIN
  1
  SerLeuIleTnTTPaAnIle 7
  |||||
  343 TCTCTCATTTACCTGGATATTT 363
Alignment Scores:
  Pred. No.: 8.85e+03 Length: 1089
  Score: 38.00 Matches: 7
  Percent Similarity: 100.0% Conservative: 0
  Best Local Similarity: 100.0% Mismatches: 0
  Query Match: 100.0% Indels: 0
  DB: 11 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x DQ049205 (1-1089)
QY 1 SerLeuIleTnTTPaAnIle 7
  |||||
  343 TCTCTCATTTACCTGGATATTT 363
RESULT 142
DQ049206 1089 bp DNA linear GSS 02-JUN-2005
LOCUS Pan troglodytes TTRAP gene, VIRUTUAL TRANSCRIPT, partial sequence,
DEFINITION Genomic survey sequence.
ACCESSION DQ049206
VERSION DQ049206.1 GI:66902405
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Pan.
          1 (bases 1 to 1089)
          Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
          Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
          White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
          A Scan for positively selected genes in the genomes of Humans and
          Chimpanzees
          (et) PLOS Biol. 3 (6), E170 (2005)
JOURNAL
  15869325
REFERENCE
  1 (bases 1 to 1089)
  Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
  Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
  White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
  Direct Submision
  Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
  Rockville, MD 20850, USA
  This sequence was made by sequencing genomic exons and ordering
  them based on alignment. Translation starts at the beginning of
  alignment.
FEATURES
  source
    1..1089
    /organism="Pan troglodytes"
    /mol_type="genomic DNA"
    /db_xref="taxon:9598"
    <1..1089
    /gene="TTRAP"
    /locus_tag="HC17203"
ORIGIN
  1
  SerLeuIleTnTTPaAnIle 7
  |||||
  343 TCTCTCATTTACCTGGATATTT 363
Alignment Scores:
  Pred. No.: 8.85e+03 Length: 1089
  Score: 38.00 Matches: 7
  Percent Similarity: 100.0% Conservative: 0
  Best Local Similarity: 100.0% Mismatches: 0
  Query Match: 100.0% Indels: 0
  DB: 11 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x DQ049206 (1-1089)
QY 1 SerLeuIleTnTTPaAnIle 7
  |||||
  343 TCTCTCATTTACCTGGATATTT 363
RESULT 143
BM555041 1103 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6545705 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737150
DEFINITION 5', mRNA sequence.
ACCESSION BM555041
VERSION BM555041.1 GI:18795166
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
          1 (bases 1 to 1103)
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgabs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNLN at:
          http://image.llnl.gov
          Plate: LHAM2746 row: m column: 23
          High quality sequence stop: 678.
          Location/Qualifiers
            1..1103
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5737150"
            /tissue_type="duodenal adenocarcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_id="NIH_MGC_88"
            /note="Organ: small intestine; Vector: PCMV-SPORE6;
            site 1: NotI; site 2: SalI; Cloned unidirectionally;
            oligo-dT primed. Average insert size 1.767 kb. Library
            enriched for full-length clones and constructed by Life

```

```

Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submision
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
  source
    1..1089
    /organism="Pan troglodytes"
    /mol_type="genomic DNA"
    /db_xref="taxon:9598"
    <1..1089
    /gene="TTRAP"
    /locus_tag="HC17203"
ORIGIN
  1
  SerLeuIleTnTTPaAnIle 7
  |||||
  343 TCTCTCATTTACCTGGATATTT 363
Alignment Scores:
  Pred. No.: 8.85e+03 Length: 1089
  Score: 38.00 Matches: 7
  Percent Similarity: 100.0% Conservative: 0
  Best Local Similarity: 100.0% Mismatches: 0
  Query Match: 100.0% Indels: 0
  DB: 11 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x DQ049206 (1-1089)
QY 1 SerLeuIleTnTTPaAnIle 7
  |||||
  343 TCTCTCATTTACCTGGATATTT 363
RESULT 143
BM555041 1103 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6545705 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737150
DEFINITION 5', mRNA sequence.
ACCESSION BM555041
VERSION BM555041.1 GI:18795166
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
          1 (bases 1 to 1103)
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgabs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNLN at:
          http://image.llnl.gov
          Plate: LHAM2746 row: m column: 23
          High quality sequence stop: 678.
          Location/Qualifiers
            1..1103
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5737150"
            /tissue_type="duodenal adenocarcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_id="NIH_MGC_88"
            /note="Organ: small intestine; Vector: PCMV-SPORE6;
            site 1: NotI; site 2: SalI; Cloned unidirectionally;
            oligo-dT primed. Average insert size 1.767 kb. Library
            enriched for full-length clones and constructed by Life

```

ORIGIN Technologies. Note: this is a NIH_MGC Library."

Alignment Scores: 8.99e+03 Length: 1103
 Pred. No.: 38.00 Matches: 7
 Score: 100.04 Conservative: 0
 Percent Similarity: 100.04 Mismatches: 0
 Best Local Similarity: 100.04 Indels: 0
 Query Match: 100.04 Gaps: 0
 DB: 3

US-10-757-745-2_COPY_115_121 (1-7) x BM555041 (1-1103)

QY 1 Serleuilethrtypasnlle 7
 Db 372 TCTCTCATTAACCTGGAATATT 392

RESULT 144

CR601303 1168 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CS0DM005YIN02 of Adult brain of Homo sapiens
 DEFINITION (human).

ACCESSION CR601303.1 GI:50482110
 VERSION HTC; CNSLT_CDNA.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1 (bases 1 to 1168)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1168)

REFERENCE Genoscope.
 AUTHORS Direct Submision
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
 REMARK - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

FEATURES Location/Qualifiers
 source 1..1168

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DM005YIN02"
 /tissue_type="Adult brain"
 /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores: 9.62e+03 Length: 1168
 Pred. No.: 38.00 Matches: 7
 Score: 100.04 Conservative: 0
 Percent Similarity: 100.04 Mismatches: 0
 Best Local Similarity: 100.04 Indels: 0
 Query Match: 100.04 Gaps: 0
 DB: 4

US-10-757-745-2_COPY_115_121 (1-7) x CR601303 (1-1168)

QY 1 Serleuilethrtypasnlle 7
 Db 368 TCTCTCATTAACCTGGAATATT 388

RESULT 145

BM553049

LOCUS 1192 bp mRNA linear EST 20-FEB-2002
 AGENCOURT 6542413 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742798
 5', mRNA sequence.

ACCESSION BM553049
 VERSION BM553049.1 GI:18791437
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1 (bases 1 to 1192)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12761 row: 1 column: 07
 High quality sequence stop: 747.

FEATURES Location/Qualifiers
 source 1..1192

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742798"
 /tissue_type="medulla"
 /lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

ORIGIN

Alignment Scores: 9.86e+03 Length: 1192
 Pred. No.: 38.00 Matches: 7
 Score: 100.04 Conservative: 0
 Percent Similarity: 100.04 Mismatches: 0
 Best Local Similarity: 100.04 Indels: 0
 Query Match: 100.04 Gaps: 0
 DB: 3

US-10-757-745-2_COPY_115_121 (1-7) x BM553049 (1-1192)

QY 1 Serleuilethrtypasnlle 7
 Db 400 TCTCTCATTAACCTGGAATATT 420

RESULT 146

CR592636 1620 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CS0DM007Y1E1 of Fetal liver of Homo sapiens
 DEFINITION (human).

ACCESSION CR592636
 VERSION CR592636.1 GI:50473443
 KEYWORDS HTC; CNSLT_CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 Homidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessée, J. and Polayès, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Peng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1620)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Séquençage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1. 1620
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODM007YE11"
/tissue_type="Fetal liver"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1.42e+04 Length: 1620
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CR592636 (1-1620)
OY 1 SerLeuIleThrTPAsnIle 7
Db 286 TCTCTCATTAACCTGGATATT 306
RESULT 147
CR602029 1743 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSOD1042YL19 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR602029.1 GI:50482836
VERSION HTC; CNGSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 1743)
REFERENCE 1 Li, W.B., Gruber, C., Jessée, J. and Polayès, D.
AUTHORS Full-length cDNA libraries and normalization
TITLE Unpublished
JOURNAL Contact : Peng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1743)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Séquençage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.
FEATURES
source
1. 1743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1042YL19"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1.55e+04 Length: 1743
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CR602029 (1-1743)
OY 1 SerLeuIleThrTPAsnIle 7
Db 212 TCTCTCATTAACCTGGATATT 232
RESULT 148
CR597293 1894 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODK007YK05 of HeLa cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR597293
VERSION CR597293.1 GI:50478100
KEYWORDS HTC; CNGSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 1894)
REFERENCE 1 Li, W.B., Gruber, C., Jessée, J. and Polayès, D.
AUTHORS Full-length cDNA libraries and normalization
TITLE Unpublished
JOURNAL Contact : Peng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1894)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Séquençage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1. 1894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK007YK05"
/tissue_type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1.71e+04 Length: 1894
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CRS97293 (1-1894)

QY 1 SerLeulleThrTyrPasnle 7
 DB 361 TCTTCATTCACCTGGAAATATT 381

RESULT 149
 CRS95644 1909 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CS0D1052YN13 of Placenta Cot 25-normalized
 DEFINITION of Homo sapiens (human)
 ACCESSION CRS95644
 VERSION CRS95644.1 GI:50476451
 KEYWORDS HTC; CDSUT_cDNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 1909)
 Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Peng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1909)
 Genoscope.
 Direct Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
 BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
 - Web: www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen

FEATURES
 source
 1..1909
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1052YN13"
 /issue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.73e+04 Length: 1909
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 4 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CRS95644 (1-1909)

QY 1 SerLeulleThrTyrPasnle 7
 DB 367 TCTTCATTCACCTGGAAATATT 387

RESULT 150
 CN164099 181 bp mRNA linear EST 02-APR-2004
 LOCUS 994218 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION CN164099
 VERSION CN164099.1 GI:46178529
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

REFERENCE
 1 (bases 1 to 181)
 Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
 Noneman, D.J., Wray, J.E. and Keefe, J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: TMM8062 row: L column: 14
 Seq primer: GTAATACGACCTGCAATATAGG.

FEATURES
 source
 1..181
 Location/Qualifiers
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="PH10B"
 /clone_lib="MARC 4PIG"
 /note="vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN
 Alignment Scores:
 Pred. No.: 1.64e+03 Length: 181
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN164099 (1-181)

QY 1 SerLeulleThrTyrPasnle 7
 DB 70 AGTTGGTCACCTGGAAATATT 90

RESULT 151
 CN164315 181 bp mRNA linear EST 02-APR-2004
 LOCUS 994602 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
 ACCESSION CN164315
 VERSION CN164315.1 GI:46178745
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 1 (bases 1 to 181)
 Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
 Noneman, D.J., Wray, J.E. and Keefe, J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: TMM8062 row: L column: 14

FEATURES
Seq primer: TAGAAGCAGCAGTCGAGC.
Location/Qualifiers
1. 181
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_11b="MARC 4PIG"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+03 Length: 181
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 05.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN164315 (1-181)

QY
1 SerLeu1eThrTTPaen1le 7
|||||:|||||:|||||
112 AGTTGTCCTCGAATATT 92

RESULT 152
AA658041 354 bp mRNA linear EST 03-DEC-1997
LOCUS AA658041/c
DEFINITION nulf03.s1 NCI CGAP Pr2 Homo sapiens CDNA clone IMAGE:1208093
similar to contains Alu repetitive element; mRNA sequence.
ACCESSION AA658041
VERSION AA658041.1 GI:2594195
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strauberg, Ph.D.
Email: cgaapb-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuangui, M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNMI at:
www.bio.lnmi.gov/bbrp/image/image.html
Insert Length: 617 Std Error: 0.00
Seq primer: -40m13 fwd: ER from Amerham.
Location/Qualifiers
1. 354
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1208093"
/sex="Male"
/dev stage="45 years old"
/lab_host="DH10B"
/clone_11b="NCI CGAP Pr2"
/note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st strand CDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial

neoplasia 2 (PIN2) cells. Double-stranded CDNA was ligated to EcoRI adaptor, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDE-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Kitzman."

ORIGIN
Alignment Scores:
Pred. No.: 3.66e+03 Length: 354
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AA658041 (1-354)

QY
1 SerLeu1eThrTTPaen1le 7
|||||:|||||:|||||
200 TCTCTGTACTCGAATATT 180

RESULT 153
CR462749 354 bp mRNA linear EST 01-JUL-2004
LOCUS CR462749
DEFINITION Rat pBluescript L10n Rattus norvegicus CDNA clone
L10NP463C02133 3', mRNA sequence.
ACCESSION CR462749
VERSION CR462749.1 GI:49595098
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
1 (bases 1 to 354)
Schuette, J., Hermann, J., Kranz, H., Loebbert, R., Schlueter, T., Schuette, D., Weindel, M., Hell, O., Ebert, L., Neubert, P., Peters, M., Radele, U., Schneider, D. and Korn, B.
Rat ArrayTAG CDNA
Unpublished (2004)
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; L10NP463C02133.
RZPDLIB;
Rat ArrayTAG CDNA
http://www.rzpd.de/cgi-bin/products/show.lib.pl.cgi?response?libNo=463 Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: RP: CAGGAACAGCTATGAC.
Location/Qualifiers
1. 354
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="L10NP463C02133"
/lab_host="DH10B"
/clone_11b="Rat pBluescript L10n"

ORIGIN
Alignment Scores:
Pred. No.: 3.66e+03 Length: 354
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.fst

Page 70

JOURNAL
COMMENT

Unpublished (2003)
Contact: Longfao Wu
Experimental Marine Biology Laboratory (EMBL)
Institute of Oceanology, Chinese Academy of Science (IOCAS)
7 Nanhai Road, Qingdao, Shandong 266071, P. R. China
Tel: +86-0532-2898552
Email: lshong@eml.ac.cn
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES
source

1..404
/organism="Argopecten irradians"
/mol_type="mRNA"
/db_xref="taxon:11199"
/sex="hermaphrodite"
/tissue_type="whole body"
/dev_stage="maturation phage"
/clone_1ib="Bay scallop uni-ZAP XR Expression Library"
/note="Organ: whole body; Vector: pBluescript(+/-)";
Site 1: XhoI; Site 2: ScaRI; Using Stratagene's Uni-ZAP XR
cDNA synthesis kit, we constructed a cDNA library of Bay
scallop. 4975 ESTs were gained."

ORIGIN

Alignment Scores:

Pred. No.: 4.28e+03 Length: 404
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CH413283 (1-404)

QY 1 SerleuileThTPaenile 7

DB 85 TCCTTATCAGCTGGAATGTA 105

RESULT 157

BZ202954 427 bp DNA linear GSS 11-OCT-2002
BZ202954/c CH230-399H1.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
DEFINITION CH230-399H1, genomic survey sequence.
ACCESSION BZ202954
KEYWORDS GSS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE

1 (bases 1 to 427)
Zhao S, Shetty J, Shatman S, Tsegaye G, Geer K, Shvartsbeyn A, Gebreyes E, Overton L, Russell D, Chen D, Riggs P, de Jong P, and Fraser C M. RABAC: Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)
Other GSS: CH230-399H1.TV
Contact: Shaying Zhao
Department of Rukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact pletier de Jong (pdejong@tigr.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ordering information.htm). BAC end
pages: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seq primer: 77
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..427
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SNHed/MCM"
/db_xref="taxon:10116"
/clone="CH230-399H1"
/sex="female"
/cell_type="brain"
/clone_1ib="CHORI-230 Segment 2"
/note="Vector: pBluescript(+/-) Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SNHed/MCM) BAC library produced by
Pletier de Jong"

ORIGIN

Alignment Scores:

Pred. No.: 4.57e+03 Length: 427
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BZ202954 (1-427)

QY 1 SerleuileThTPaenile 7

DB 159 TCACCTGCTGACCTGGAACATC 139

RESULT 158

AA427279 440 bp mRNA linear EST 16-OCT-1997
V447911.61 Knowles Solter mouse 2 cell Mus musculus cDNA clone
LOCUS IMAGE:803780 5', mRNA sequence.
DEFINITION AA427279.1 GI:2110084
ACCESSION AA427279
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 440)
Marras M, Hillier L, Allen M, Bowles M, Dietrich N, Dubuque T, Geisel S, Kucaba T, Lacy M, Le M, Martin J, Morris M, Scheinberg R, Steptoe M, Tan F, Underwood K, Moore B, Theising B, Wylie T, Lennon G, Soares B, Wilson R, and Waterston R. The WashU-HMI Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 266 1800
Fax: 314 266 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:480124
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
1..440
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:803780"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pBluescribe (modified);

Site 1: MluI; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI(dT): 5'-CGATCGACGTCGACCGTGTGTGT-3'. CDNAS were cloned into the MluI/SalI sites of a modified Bluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

ORIGIN

Alignment Scores:

Pred. No.:	4,74e+03	Length:	440
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x AA427279 (1-440)

QY 1 SerLeuIeThrTPaSnIle 7

DB 258 TCTTGTGCACATGGAACATA 238

RESULT 159

LOCUS A0613212/c 454 bp DNA linear GSS 15-JUN-1999

DEFINITION HS_5133_A1_G02_SPEE_RPCT-11 Human Male BAC library Homo sapiens genomic clone Plate=709 Col=3 Row=M, genomic survey sequence.

ACCESSION A0613212

VERSION A0613212.1 GI:5074488

KEYWORDS GSS.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 454)

Mahiraes,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

Contact: Mahiraes CG, Wallace JC, Hood L

High Throughput Sequencing Center

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCT-11. For BAC

library availability, please contact Pletier de Jong (pletier@u.washington.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.uh.edu/ordering_bac.html) or from Research Genetics (<http://www.hresc.washington.edu>). BAC end Web Server: <http://www.hresc.washington.edu>

Plate: 709 row: M column: 3

Seq primer: SPE

Classes: BAC ends

High quality sequence start: 454.

Location/Qualifiers

1..454

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone_1ib="Plate=709 Col=3 Row=M"

/sex="male"

/clone_1ib="RPCT-11 Human Male BAC library"

/note="Vector: PBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the PBACe3.6 vector at EcoRI sites"

ORIGIN

Alignment Scores:

Pred. No.:	4,92e+03	Length:	454
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	9	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x A0613212 (1-454)

QY 1 SerLeuIeThrTPaSnIle 7

DB 203 AGCTPAGTACATGGAATATC 183

RESULT 160

LOCUS BE836176/c 455 bp mRNA linear EST 22-SEP-2000

DEFINITION PM4-FN0057-100600-001-cl1 FN0057 Homo sapiens CDNA, mRNA sequence.

ACCESSION BE836176

VERSION BE836176.1 GI:10268554

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 455)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2=PM4-FN0057-100600-001-cl1&t3=2000-06-10&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 3

High quality sequence stop: 455.

Location/Qualifiers

1..455

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_1ib="FN0057"

/note="Organ: prostate_normal; Vector: puc18; Site 1:

Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	4,93e+03	Length:	455
Score:	37.00	Matches:	6

Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BE836176 (1-455)

QY 1 SerleuileThrtPanille 7
 |||||:|||||
 47 TCTCTGTCAATGAGATGTA 27

RESULT 161
 CB415942 471 bp mRNA linear EST 01-JAN-2005
 LOCUS CB415942
 Scaf.5865 Bay scallop Uni-ZAP XR Expression Library, Argopecten
 Definition Irradians cDNA 5' similar to Argopecten irradians similar to
 Metridium senile Cam mRNA for calmodulin, partial cds, mRNA
 sequence.

ACCESSION CB415942 GI:56937503
 VERSION CB415942.1
 KEYWORDS EST
 SOURCE Argopecten irradians
 ORGANISM Argopecten irradians
 Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 Pectinoidea; Pectinidae; Argopecten.

REFERENCE 1 (bases 1 to 471)
 Song, L., Xu, W., Li, H., Wu, L., Xiang, J. and Guo, X.
 The construction and EST analysis of cDNA library from bay scallop
 Argopecten irradians
 Unpublished (2003)

JOURNAL Contact: Longtao Wu
 Experimental Marine Biology Laboratory (EMBL)
 Institute of Oceanology, Chinese Academy of Science (IOCAS)
 7 Nanhai Road, Qingdao, Shandong 266071, P. R. China
 Tel: +86-0532-2898552
 Email: lshsongemqdio.ac.cn
 Seq primer: M13 Forward.

FEATURES
 Location/Qualifiers
 1..471
 /organism="Argopecten irradians"
 /mol_type="mRNA"
 /db_xref="taxon:31199"
 /sex="hermaphrodite"
 /tissue_type="whole body"
 /dev_stage="maturation phase"
 /clone_lib="Bay scallop Uni-ZAP XR Expression Library"
 /note="Organ: whole body; Vector: pBluescript (+/-);
 Site 1: XhoI; Site 2: EcoRI; Using Stratagene's Uni-ZAP XR
 cDNA synthesis kit, we constructed a cDNA library of Bay
 scallop. 4975 ESTs were gained."

ORIGIN

Alignment Scores:
 Pred. No.: 5.14e+03 Length: 471
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CB415942 (1-471)

QY 1 SerleuileThrtPanille 7
 |||||:|||||
 270 TCTTATCATCGTGAATGTA 290

RESULT 162
 BI275343 501 bp mRNA linear EST 18-JUL-2001
 LOCUS BI275343
 Definition UI-R-CXO-bmw-d-04-0-UI-s1 UI-R-CXO Rattus norvegicus cDNA clone
 UI-R-CXO-bmw-d-04-0-UI 3', mRNA sequence.

ACCESSION BI275343 GI:14887105
 VERSION BI275343.1

KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Carnata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 501)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Gene Res. 6 (9), 791-806 (1996)

JOURNAL Contact: Soares, MB
 PUBMED 8889546
 COMMENT Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newcom Road, 4156 MEBR, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized rat placenta pool library cDNA library preparation. M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
 Location/Qualifiers
 1..501
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CXO-bmw-d-04-0-UI"
 /dev_stage="ADULT"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-CXO"
 /note="Vector: pUT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CXO
 library is a normalized library constructed from the
 following rat placenta tissues: embryonic day 17,
 embryonic day 19, embryonic day 21. For a detailed
 description of the library from which this clone was
 derived, please visit our web site at
 ratresg.uiowa.edu. The subtraction has been previously
 described in (Bonaldo, Lennon and Soares, Genome Research
 6:791-806, 1996)
 TAG_TISSUE=rat placenta pool
 TAG_LIB=UI-R-CXO
 TAG_SEQ="TCACGACACTG"

ORIGIN

Alignment Scores:
 Pred. No.: 5.53e+03 Length: 501
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BI275343 (1-501)

QY 1 SerleuileThrtPanille 7
 |||||:|||||
 344 TCTTGTCAATGAGACATA 364

RESULT 163
 AA591859 504 bp mRNA linear EST 16-SEP-1997
 LOCUS AA591859/c
 Definition VK9107.01 Knowles Solter mouse 2 cell Mus musculus cDNA clone
 IMAGE:962077 5', mRNA sequence.

ACCESSION AA591859
 VERSION AA591859.1 GI:2405522
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 504)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenger, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HM Mouse EST Project
 Unpublished (1996)
 CONTACT: Marra M/Mouse EST Project
 WashU-HM Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LML: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:550869
 High quality sequence stop: 491.
 Location/Qualifiers
 1..504
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J x DBA/2J F1"
 /db_xref="taxon:10090"
 /clone="IMAGE:962077"
 /issue_type="embryo"
 /dev_stage="2-cell"
 /lab_host="DH10B"
 /clone_lib="Knowles Solter mouse 2 cell"
 /note="Organ: embryo; Vector: pluscscribe (modified); Site 1: MluI; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI(dT): 5'-CGGTGACGCGTGGCGCTTTTCTTTT-3', CDNA: were cloned into the MluI/SalI sites of a modified pluscscribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.57e+03 Length: 504
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 1 Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x AA591859 (1-504)
 QY 1 SerLeuileThrTPanille 7
 DB 258 TCTTGTGTCATGGAACATA 238
 RESULT 164
 LOCUS BE107896 545 bp mRNA linear EST J3-JUN-2000
 DEFINITION UI-R-CAO-awy-a-11-0-UI.81 UI-R-CAO Rattus norvegicus cDNA clone
 BE107896
 UI-R-CAO-awy-a-11-0-UI 3', mRNA sequence.
 BE107896.1 GI:8500001
 EST.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE 1
 AUTHORS Bonaldi, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 COMMENT 8889548
 CONTACT: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized cerebellum library cDNA library preparation: M.B. Soares lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
 Seg primer: M13 Forward
 POLYA=yes.
 Location/Qualifiers
 1..545
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CAO-awy-a-11-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-CAO"
 /note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI. The UI-R-CAO library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratent.eng.uiowa.edu. The subtraction has been previously described in (Bonaldi, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_TISSUE=cerebellum
 TAG_LIB=UI-R-CAO
 TAG_SEQ=CGGAAC
 ORIGIN
 Alignment Scores:
 Pred. No.: 6.12e+03 Length: 545
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 2 Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x BE107896 (1-545)
 QY 1 SerLeuileThrTPanille 7
 DB 343 TCTTGTGTCATGGAACATA 363
 RESULT 165
 LOCUS CE565005 585 bp DNA linear GSS 28-SEP-2003
 DEFINITION t1gr-gss-dog-17000312704632 dog library Canis familiaris genomic,
 CE565005
 genomic survey sequence.
 CE565005.1 GI:36881786
 GSS.
 Canis familiaris (dog)
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 585)
Kirkness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M., and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
1451627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: Shotgun.
Location/Qualifiers
1..585
/organism="Canis familiaris"
/mol_type="Genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: Back; Libraries were prepared from
peripheral blood"

ORIGIN

Alignment Scores:

Pred. No.:	6,65e+03	Length:	585
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	10	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CF565005 (1-585)

QY 1 Serleu1eThrTPaen1e 7
|||||
Db 575 AGCCTGATCACTGGATGTA 555

RESULT 167
CN782353 603 bp mRNA linear EST 21-MAY-2004
LOCUS
DEFINITION
a1.1004.42 Bay Scallop planktonic veliger larvae ZAP Express
Library Argopecten irradians cDNA 5' similar to Calmodulin
CG8472.2A [Diosophila melanogaster], mRNA sequence.
ACCESSION
CN782353 GI:47561814
VERSION
CN782353.1
KEYWORDS
EST
Argopecten irradians
Argopecten irradians
Bivalvia; Mollusca; Bivalvia; Periomorpha; Pectinoida;
Pectinoida; Pectinidae; Argopecten.
REFERENCE
1 (bases 1 to 603)
Roberts, S.B. and Geor, F.W.
Expressed sequence tags from early developmental stages of the bay
scallop Argopecten irradians (2004)
Unpublished (2004)
CONTACT: Roberts, SB
Program in Scientific Aquaculture
Marine Biological Laboratory
7 MBL St. Woods Hole, MA 02543, USA
Tel: 508-289-7621
Fax: 508-289-7900
Email: sroberts@mbi.edu
Seq primer: BK reverse
Location/Qualifiers
1..603
/organism="Argopecten irradians"
/mol_type="mRNA"
/db_xref="taxon:31199"

FEATURES
source

/tissue_type="whole body"
/dev_stage="planktonic veliger larvae ZAP
Express Library"
/clone_lib="Bay Scallop planktonic veliger larvae ZAP
Express Library"
/note="Vector: pBK-CMV"

ORIGIN

Alignment Scores:

Pred. No.:	6,9e+03	Length:	603
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CN782353 (1-603)

QY 1 Serleu1eThrTPaen1e 7
|||||
Db 555 TCCTTAATCACTGGATGTA 575

RESULT 167
BB619120 615 bp mRNA linear EST 26-OCT-2001
LOCUS
DEFINITION
BB619120 RIKEN full-length enriched, 8 days embryo Mus musculus
cDNA clone 5730484M20 5', mRNA sequence.
ACCESSION
BB619120
VERSION
BB619120.1 GI:16458534
KEYWORDS
EST
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 615)
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Kono, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
Riken Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
CONTACT: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagui, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.,
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamane, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, K., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with

/clone_lib="RIKEN full-length enriched, 13 days embryo lung"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCCGACACGAGTTTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGTTCTCGAGTTAATTAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FHC I."

ALIGNMENT SCORES:

Pred. No.:	7.63e+03	Length:	656
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BA485402 (1-656)

OY 1 SerLeuileThrtPAnlle 7
 |||||:|||||
 DB 332 TCTTGTGCATGACATCA 312

RESULT 171 BY740567 657 bp mRNA linear EST 17-DEC-2002
 LOCUS BY740567 RIKEN full-length enriched, 16 days embryo kidney Mus
 DEFINITION musculus cDNA clone 192008BD14 5', mRNA sequence.
 ACCESSION BY740567 GI:27164930
 VERSION BY740567.1 GI:27164930
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 657)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikiado, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bulc, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matuda, H., Batelov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochlova, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fleischer, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S., Guenincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglocz, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavani, W.J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Veierod, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wymshay-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kikukawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arahawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

TITLE
 JOURNAL
 PUBMED
 COMMENT
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-research.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi, J., Aizawa, K., Akimura, T., Arahawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source
 Location/Qualifiers
 1..657
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="192008BD14"
 /tissue_type="kidney"
 /dev_stage="16 days embryo"
 /clone_lib="RIKEN full-length enriched, 16 days embryo kidney"

ALIGNMENT SCORES:

Pred. No.:	7.64e+03	Length:	657
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BY740567 (1-657)

OY 1 SerLeuileThrtPAnlle 7
 |||||:|||||
 DB 582 TCTTGTGCATGACATCA 562

RESULT 172 BY740588 657 bp mRNA linear EST 17-DEC-2002
 LOCUS BY740588 RIKEN full-length enriched, pooled tissues, 16 days embryo, etc. Mus musculus cDNA clone 1920089C06 5', mRNA sequence.
 DEFINITION BY740588
 ACCESSION BY740588 GI:27164963

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Eumarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 657)

TITLE
JOURNAL
PUBMED
COMMENT

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

CONTACT: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-resseqc.riken.jp, URL: http://genome-gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Horii, F.,
Imomura, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Okazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, K.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-285 (2001)
A cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues
Please visit our web site (http://genome-gsc.riken.go.jp) for
further details
Location/Qualifiers

SOURCE

1. 657
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="1920089C06"
/clone_11b="RIKEN full-length enriched, pooled tissues, 16
days embryo, etc."
/note="pooled tissues (dev_stage=16 days
embryo, tissue_type=heart, sex=mix), (dev_stage=16 days
embryo, tissue_type=kidney, sex=mix), (dev_stage=17 days
embryo, tissue_type=heart, sex=mix), (dev_stage=17 days
embryo, tissue_type=stomach, sex=mix), (dev_stage=17 days
embryo, tissue_type=kidney, sex=mix), (dev_stage=17 days
pregnant, adult, tissue_type=amolon, sex=female)"
(dev_stage=13 days embryo, tissue_type=liver, sex=mix)"

ORIGIN

Alignment Scores:
Pred. No.: 7,64e+03 Length: 657
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BY740588 (1-657)

QY

1 SerLeuIleThrTPAsnIle 7

DB

509 TCTTGTGCATGAGACATA 489

RESULT 173

BB616066/c 658 bp mRNA linear EST 26-OCT-2001
LOCUS BB616066 RIKEN full-length enriched, adult male testis Mus musculus

DEFINITION

cDNA clone 4931404P18.5', mRNA sequence.

ACCESSION

BB616066

VERSION

BB616066.1 GI:16456257

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Eumarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hirozane, K., Horii, F., Ishii, Y., Ito, M., Kawai, J.,
Kondo, S., Kono, H., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216

TITLE

JOURNAL

COMMENT

Email: genome-resseqc.riken.jp, URL: http://genome-gsc.riken.jp/
Carninci, P., Shibata, K., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Tozawa, Y., Tanaka, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Otsawa, K., Izawa, T.,
Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.


```

DB: 2 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BB660102 (1-660)
OY 1 Serleu1lethrrTPpanille 7
Db 517 TCTTTGGTCACATCGAAGCTA 497

RESULT 175
CC432105 661 bp DNA linear GSS 20-MAY-2003
LOCUS CC432105
DEFINITION genomic survey sequence.
ACCESSION CC432105
VERSION CC432105.1 GI:30927633
KEYWORDS GSS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PNCMD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 661)
Whiteley C.A., Quackenbush J., Van Aken S., Utecher B.T.,
Benner C.A., Fraser, C.M., Xian, Y., San Miguel, P., Ma, J. and
Maize Genomics Consortium
Unpublished (2003)
Other GSS: PNH0727B
Contact: Cathy Whiteley
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteley@tigr.org
Seq primer: TP
Classes: sheared ends.

FEATURES
source
1..661
location/Qualifiers
1..organism="Zea mays"
1..mol_type="genomic DNA"
1..strain="B73"
1..DB_xref="taxon:4577"
1..clone_lib="ZMBR453123"
1..clone_id="ZM_0.6_1.0_KB"
1..note="vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"

Alignment Scores:
Pred. No.: 7.7e+03
Score: 37.00 Length: 661
Percent Similarity: 100.0% Matches: 6
Best Local Similarity: 85.7% Mismatches: 1
Query Match: 97.4% Indels: 0
Gaps: 0
DB: 9

US-10-757-745-2_COPY_115_121 (1-7) x CC432105 (1-661)
OY 1 Serleu1lethrrTPpanille 7
Db 361 TCACGTGATCAGCTGGAATGTA 381

RESULT 176
BI664350/c 669 bp mRNA linear EST 18-SEP-2001
LOCUS BI664350/c
DEFINITION mRNA sequence.
ACCESSION BI664350
VERSION BI664350.1 GI:15646978
KEYWORDS EST.
SOURCE
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciuromorphi; Murioidea; Muridae; Murinae; Mus.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS 1 (bases 1 to 669)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strusberg, Ph.D.
 Email: sgabbs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL1874 row: k column: 22
 High quality sequence stop: 669.
 Location/Qualifiers
 1..669
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5344269"
 /sex="female"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="VDH08"
 /clone_id="NCI CGAP Mam6"
 /note="Organ: Mammary; Vector: PCMV-SPORT6; Site:1; Salt;
 Site:2; Nof1; Cloned unidirectionally. Primer: Oligo dr.
 library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Alignment Scores:
 Pred. No.: 7.81e+03 Length: 669
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1604350 (1-669)

Dy 1 SerleuileThrTyrphenlle 7
 Qy |||||:|||||
 S17 TCTTGGTCACATGAAACATA 497

RESULT 177

DE065860
 LOCUS DE065860 669 bp DNA linear GDS 25-MAY-2005
 DEFINITION Oryzias latipes DNA, clone: Olal-160B09.F, genomic survey sequence.
 VERSION DE065860.1 GI:62577424
 KEYWORDS GSS.
 SOURCE Oryzias latipes (Japanese medaka)
 ORGANISM Oryzias latipes
 Buxarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorphi; Acanthopterygii; Percomorphi; Atherinomorpha;
 Belontiiformes; Atherinichthyidae; Oryziinae; Oryzias.
 1
 Fujiyama,A., Toyoda,A., Kuroki,Y. and Sakaki,Y.
 BAC end sequences of Olal Oryzias latipes library
 JOURNAL Published Only in Database (2005)
 2 (bases 1 to 669)
 Fujiyama,A.
 DIRECT SUBMISSION
 Submitted (12-Apr-2005) Aaso Fujiyama, The Institute of Physical
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 (E-mail: fujiyama@gsc.riken.jp, URL: http://etc.gsc.riken.jp/

COMMENT Tel:81-3-4212-2558, Fax:81-3-3556-1916)
This work was done in collaboration with Takeda, H. (1), Naruse, K. (2)

and Narita, T. (3)
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E-mail: tanarita.s.u-tokyo.ac.jp

PRIMERS

Sequencing : Forward

LIBRARY

Vector : pKS145
R.Site 1 : SacI
L.Site 2 : SacI.

FEATURES

source

Location/Qualifiers
1..669
/organism="Oryzias latipes"
/mol_type="genomic DNA"
/db_xref="taxon:8090"
/clone="Olai-160B09.F"
/sex="male"
/cell_type="whole body"
/clone_lib="BAC end sequences of Olai Oryzias latipes library"

ORIGIN

Alignment Scores:
Pred. No.: 7.81e+03 Length: 669
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x DE065880 (1-669)

OY 1 Serleu1eThrTPanille 7
Db 179 AGCCTCGACGTGAGATATT 199

RESULT 178 668 bp mRNA linear EST 26-JUL-2002
B0769225/c
LOCUS B0769225
DEFINITION IMAGE:5720609 5', mRNA sequence.

ACCESSION B0769225
VERSION B0769225.1 GI:21977699
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 688)
NIH-MGC http://mgi.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: PYX-5.

FEATURES

source

Location/Qualifiers
1..688
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5720609"
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH BMAP_FCO"
/note="Organ: brain; Vector: PYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into PYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is TGAAGAGCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 8.07e+03 Length: 688
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B0769225 (1-688)

OY 1 Serleu1eThrTPanille 7
Db 28 TCTTTGTCACATGACATA 8

RESULT 179 694 bp mRNA linear EST 17-DEC-2002
BY748935/c
LOCUS BY748935
DEFINITION BY748935 RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus cDNA clone F63021A16 5', mRNA
Sequence.

ACCESSION BY748935
VERSION BY748935.1 GI:27178043
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 694)
Kazaki, Y., Furuno, M., Kaubawa, T., Adachi, J., Bono, H.,
Nikaido, I., Otsu, N., Saio, R., Suzuki, H., Yamakawa, T.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schirral, L. M., Kanapin, A., Macaula, H.,
Batalov, S., Betzel, K. W., Blake, J. A., Bradt, D., Brusic, V.,

Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaetecland, T., Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S., Gustlich, S., Hitokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglocz, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mik, H., Nagshima, T., Numata, K., Okido, T., Pavani, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takemata, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Varado, R., Wagner, L., Wnshaw-Boris, A., Yamagisawa, M., Yang, I., Wells, C., Wilming, L.G., Wnshaw-Boris, A., Yamagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carrini, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, U., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

1246851

TITLE
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9226

JOURNAL
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, U., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, U., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohse, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.

COMMENT
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichipillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES
source
1. 694
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630217A16"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_11p="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells"

ORIGIN
Alignment Scores:
Pred. No.: 8.1e+03 Length: 694
Score: 57.00 Matches: 5
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 85.7% Indels: 1
Query Match: 97.4% Gaps: 0
DB: 5

US-10-757-745-2_COPY_115_121 (1-7) x BY48935 (1-694)

OR
1 SerLeuIleTTTPanille 7
|||||
DB 528 TCCTTGTGTCACATGAAACATA 508

RESULT 180
BQ179160/c 702 bp mRNA linear EST 30-APR-2002
LOCUS
BQ179160/c
DEFINITION
UT-M-EMO-bwa-k-23-0-UT-r1 NIH_BMAP_EMO Mus musculus cDNA clone
IMAGE:5703310 5', mRNA sequence.

ACCESSION
BQ179160
BQ179160.1 GI:20354652

VERSION
EST.

KEYWORDS
Mus musculus (house mouse)

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, U., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohse, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Unpublished (1999)

JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
RISSE Procurement: Dr. James Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA library arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILN at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
source
Seq primer: pyx-5.
1. 702
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5703310"
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/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_11b="NIH_BMAP_EMO"
/note="Organ: brain; Vector: pyx-Asc; Site: 1; Ecor I; Site: 2; Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	8,27e+03	Length:	702
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BQ179160 (1-702)

Qy 1 Serleuilethrtipansnle 7

Db 518 TCTTGTGCATCGAACATA 498

RESULT 181 BU053419 712 bp mRNA linear EST 26-AUG-2002

LOCUS BU053419/c UI-M-FCO-bzd-k-13-0-UI.r1 NIH BMAP_FCO Mus musculus cDNA clone

DEFINITION IMAGE:6402180 5', mRNA sequence.

ACCESSION BU053419 GI:22493496

VERSION BU053419.1 GI:22493496

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgs.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/BLN at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

FEATURES

source

1..712 Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6402180"

/tissue_type="whole brain"

/dev_stage="embryo 12.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_1ib="NIH BMAP FCO"

/note="Organ: brain; Vector: pYX-asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-asc vector. The library tag sequence located between the Not I site and the polyA tail, is TAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores: 8.41e+03 Length: 712

Pred. No.:

Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU053419 (1-712)

Qy 1 Serleuilethrtipansnle 7

Db 525 TCTTGTGCATCGAACATA 505

RESULT 182 BY741565/c

LOCUS BY741565 RIKEN full-length enriched, B16 F10Y cells Mus musculus

DEFINITION CDNA clone G370147H12 5', mRNA sequence.

ACCESSION BY741565

VERSION BY741565.1 GI:27166545

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgs.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/BLN at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

FEATURES

source

1..712 Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6402180"

/tissue_type="whole brain"

/dev_stage="embryo 12.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_1ib="NIH BMAP FCO"

/note="Organ: brain; Vector: pYX-asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-asc vector. The library tag sequence located between the Not I site and the polyA tail, is TAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores: 8.41e+03 Length: 712

Pred. No.:

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Cells were provided by Drs. William J Pavan, Stacie Loftus, and Denise Larson (Division of Intramural Research Genetic Disease Research Branch National Human Genome Research Institute, National Institutes of Health (NIH) Building 49, Room 4A82 49 Convent Drive MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
1..713
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370147H12"
/cell_type="B16 F10Y cells"
/clone_11b="RIKEN full-length enriched, B16 F10Y cells"

ORIGIN

Alignment Scores:

Pred. No.: 8.43e+03 Length: 713
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BY741565 (1-713)

QY 1 SerLeuIleThrTPaenIle 7
|||||:|||||
527 TCTTGGTCACATGGAACATA 507

Db 527 TCTTGGTCACATGGAACATA 507

RESULT 183

CA132027

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CA132027 714 bp mRNA linear EST 24-SEP-2003
SCBGR1052C04.G RT1 Saccharum officinarum cDNA clone SCBGR1052C04
5' mRNA sequence:
CA132027
EST
CA132027.1 GI:35016608
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 714)
Vettore,A.L., da Silva,F.R., Kemper,F.L. and Arruda,P.
The libraries that made SUCST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

FEATURES

source

Email: parvuda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fca.unicamp.br>
Plate: 052 Row: C Column: 04
Seq primer: 17 promoter primer.
Location/Qualifiers

1..714
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCBGR1052C04"
/lab_host="DH10B"
/clone_11b="RT1"
/note="Organ: Root tips (0.3cm-long) from adult plants; Vector: pSport1; Site: Salt; Site 2: Not; An unidirectional cDNA library generated from [Root tips (0.3cm-long) from adult plants] cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNA were fractionated in a sepharose CL-2B 40cm-column and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>"

ORIGIN

Alignment Scores:

Pred. No.: 8.44e+03 Length: 714
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CA132027 (1-714)

QY 1 SerLeuIleThrTPaenIle 7
|||||:|||||
685 AGCTTAATTAACGTGAATGTT 705

Db 685 AGCTTAATTAACGTGAATGTT 705

RESULT 184

CF533524/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CF533524 715 bp mRNA linear EST 12-SEP-2003
UI-M-GHO-cgy-k-08-0-UI.r1 NIH-BMAP_GHO Mus musculus cDNA clone
IMAGE:30532759 5' mRNA sequence.
CF533524
EST
CF533524.1 GI:34585492
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 715)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bpc-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
<http://genome.iowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: PYX-5'
Location/Qualifiers
1..715
/organism="Mus musculus"
/mol_type="mRNA"

```

/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:3053759"
/tissue_type="Whole brain"
/dev stage="1, 5, and 15 days newborn"
/lab host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GH0"
/Note="Organ: Brain; Vector: pYX-Asc, Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldi, Lemmon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. Ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGACTGAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

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ORIGIN

Alignment Scores:

Pred. No.:	8.45e+03	Length:	718
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CFS3524 (1-715)

QY 1 SerLeuIeThrTPAsnIle 7
 Db 457 TCTTGTGCATGACGACATA 437

RESULT 185

CNS05S51 718 bp mRNA linear HTC 05-JUL-2005
 LOCUS Tetraodon nigroviridis full-length cDNA.
 ACCESSION CR639168
 VERSION CR639168.2 GI:56240375
 KEYWORDS HTC, cDNA: full-length, full-length cDNA, Tetraodon nigroviridis.
 SOURCE Tetraodon nigroviridis
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
 Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS Jallouf, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
 Maucell, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
 Nicud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
 Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
 Casellano, S., Anthouard, V., Ublin, C., Castell, V., Katinka, M.,
 Vacherie, B., Biemont, C., Skalli, Z., Catolico, L., Poullain, J., De
 Bernardinis, V., Cruaud, C., Duprat, S., Broctier, P., Couanceau, J.P.,
 Guay, J., Parra, G., Lardier, G., Chapelle, C., McKernan, K.J.,
 McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
 Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
 Robinson-Rechavi, M., Lauder, V., Schachter, V., Quetez, F.,
 Sautin, M., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.,
 and Roest Crolius, H.

TITLE Genome duplication in the teleost fish Tetraodon nigroviridis
 reveals the early vertebrate proto-karyotype

JOURNAL Nature 431 (7011), 946-957 (2004)
 PUBMED 15496914

REFERENCE Genoscope.
 TITLE Direct Submission
 AUTHORS 2 (bases 1 to 718)
 JOURNAL Submitted (25-Nov-2004) Genoscope - Centre National de Sequencage -

COMMENT : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 (E-mail : segefigenoscope.cns.fr - Web : www.genoscope.cns.fr)
 On Dec 3, 2004 this sequence version replaced g1:51135613.
 The sequences are based on single pass reads.
 More information available at
 http://www.genoscope.cns.fr/tetraodon.

FEATURES

source
 1..718
 /organism="Tetraodon nigroviridis"
 /mol_type="mRNA"
 /db_xref="taxon:99883"
 /tissue_type="liver"

ORIGIN

Alignment Scores:

Pred. No.:	8.5e+03	Length:	718
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	4	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CNS05S51 (1-718)

QY 1 SerLeuIeThrTPAsnIle 7
 Db 358 TCGCTGATTAACCTGACGCTG 378

RESULT 186

LOCUS BO745578 730 bp mRNA linear EST 17-JUL-2002
 DEFINITION UT-M-EMO-bxh-e-03-0-UT-r1 NIH_BMAP_EMO Mus musculus cDNA clone
 IMAGE:5708138 5', mRNA sequence.
 ACCESSION BO745578
 VERSION BO745578.1 GI:21892365
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaab@ncl.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLM at:
 http://image.llnl.gov

FEATURES
 source
 1..730
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5708138"
 /tissue_type="whole brain"
 /dev stage="embryo 15.5 dpc"
 /lab host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_EMO"
 /Note="Organ: Brain; Vector: pYX-Asc, Site_1: EcoR I;
 Site_2: Not I; The library was constructed according to
 Bonaldi, Lemmon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1..730
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5708138"
 /tissue_type="whole brain"
 /dev stage="embryo 15.5 dpc"
 /lab host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_EMO"
 /Note="Organ: Brain; Vector: pYX-Asc, Site_1: EcoR I;
 Site_2: Not I; The library was constructed according to
 Bonaldi, Lemmon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an

ORIGIN

oligo-dt primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTCGGA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
8.67e+03	37.00	100.0%	85.7%	97.4%	730	6	1	0	0	0

US-10-757-745-2_COPY_115_121 (1-7) x BQ745578 (1-730)

QY 1 SerleuileThrTyrPasn1le 7

DB 123 TCTTGTGTCACATGACACATA 103

RESULT 187

CF749729/c

LOCUS

DEFINITION

IMAGE:30627991 5', mRNA sequence.

CF749729

CF749729.1

GI:37646074

EST

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Musinae; Mus.

1 (bases 1 to 737)

NIH-MGC http://mgs.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.iowa.edu/distribution/mouseefl.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

FEATURES

source

Seq primer: PYX-5.

Location/Qualifiers

1..737

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30627991"

/tissue_type="Upper Head"

/dev_stage="9.5 and 10.5 dpc"

/lab_host="NIH BMAP HJ0"

/clone_lib="NIH BMAP HJ0"

/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according

Bonafide, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned

ORIGIN

directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACGTAAAT. This library (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH).

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
8.76e+03	37.00	100.0%	85.7%	97.4%	737	6	1	0	0	0

US-10-757-745-2_COPY_115_121 (1-7) x CF749729 (1-737)

QY 1 SerleuileThrTyrPasn1le 7

DB 339 TCTTGTGTCACATGACACATA 319

RESULT 188

CR296536/c

LOCUS

DEFINITION

IMAGE:30627991 BAC end, cultivar Jemalong A17 of Medicago truncatula,

genomic survey sequence.

CR296536

CR296536.1

GI:44690539

GSS

Medicago truncatula (barrel medic)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;

Medicago.

1 (bases 1 to 740)

Genoscope.

Direct Submission

Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage;

BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr

- web : www.genoscope.cns.fr)

Location/Qualifiers

1..740

/organism="Medicago truncatula"

/mol_type="genomic DNA"

/cultivar="Jemalong A17"

/db_xref="taxon:3880"

/clone_lib="MTL"

/note="Vector: pIndigoBAC; Site_1: EcoRI; Site_2: EcoRI

/Debelle F. and Chalhou B.

Genoscope sequence ID : mte1-13c4fm1"

FEATURES

source

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
8.81e+03	37.00	100.0%	85.7%	97.4%	740	6	1	0	0	0

US-10-757-745-2_COPY_115_121 (1-7) x CR296536 (1-740)

QY 1 SerleuileThrTyrPasn1le 7

DB 654 AGTTTGATACCTGGAATATT 634

RESULT 189

CC666503

LOCUS

DEFINITION

OG91933TH_ZM_0.7.1.5_KB Zee may genomic clone ZMMBMA0452017,

genomic survey sequence.

741 bp DNA linear GSS 19-JUN-2003

ACCESSION CC666503 GI:32070577
 VERSION CC666503.1
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 741)
 White, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other_GSSs: OCU7193TV
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@cigr.org
 Seq primer: 7R
 Classes: methylation filtered.
 Location/Qualifiers
 1..741
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="ZMMMA0452017"
 /note="Vector: pBCSK-1 Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN
 Alignment Scores:
 Pred. No.: 8.82e+03 Length: 741
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CC666503 (1-741)

Qy 1 Serleu1erhTTPasnlle 7
 |||||
 Db 162 TCACGTGATCAGCTGGAATGTA 182

RESULT 190
 CV073972/c 743 bp mRNA linear EST 25-AUG-2004
 DEFINITION AGENCOURT_31481300 NIH_MGC_251 Rattus norvegicus cDNA clone
 IMAGE:7387175 5', mRNA sequence.
 CV073972
 CV073972.1 GI:51541003
 EST.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.
 1 (bases 1 to 743)
 NIH-MGC http://mgc.nci.nih.gov/
 Unpublished (1999)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

CDNA Library Preparation: Open Biosystems
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM1555 row: h column: 21
 High quality sequence stop: 705.
 Location/Qualifiers
 1..743
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="IMAGE:7387175"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_251"
 /note="Organ: thymus; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer:
 5'-PGACTAGTCTAGATCGGAGCGGCCGC(7)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.6 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_250) and was constructed by Open Biosystems. Note: this is a NIH_MGC library"

ORIGIN
 Alignment Scores:
 Pred. No.: 8.85e+03 Length: 743
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CV073972 (1-743)

Qy 1 Serleu1erhTTPasnlle 7
 |||||
 Db 493 TCTTTGTCATGGAACATA 473

RESULT 191
 C0045302/c 747 bp mRNA linear EST 10-JUN-2004
 DEFINITION UI-M-HQ0-GFP-a-23-0-UI_r1 NIH_BMAP_HQ0 Mus musculus cDNA clone
 IMAGE:30662710 5', mRNA sequence.
 C0045302
 C0045302.1 GI:48585456
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 747)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mouse1.html
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: PYX-5.
 Location/Qualifiers
 1..747

FEATURES
 source

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30662710"
/rname_type="Upper Head"
/dev_stage="embryo 9.5 - 10.5 dpc"
/lab_host="NIH RMAP HQ"
/note="Organ: Upper Head; Vector: pYX-Asc; Site: 1; Ecor I; Site: 2; Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGACTGAAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Alignment Scores:
Pred. No.: 8.91e+03 Length: 747
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x C0045302 (1-747)

OY 1 SerleuileThrTPanille 7
Db 176 TCTTGGTCACATGGAACATA 156

RESULT 192 BZ993817 758 bp DNA linear GSS 25-MAR-2003
LOCUS BZ993817
DEFINITION Genomic survey sequence.
ACCESSION BZ993817
VERSION BZ993817.1 GI:29237234
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 758)
Whiteley, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Bennezen, J., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFJ230TD
Contact: Cathy Whiteley

TIGR
7912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteley@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source 1 location/Qualifiers
1 758
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"

/clone="ZMMBTA360F12"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPo; Site: 1; EcorI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN

Alignment Scores:
Pred. No.: 9.06e+03 Length: 758
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BZ993817 (1-758)

OY 1 SerleuileThrTPanille 7
Db 570 TCACTGATCACCCTGGAATGTA 550

RESULT 193 BZ993822 764 bp DNA linear GSS 25-MAR-2003
LOCUS BZ993822
DEFINITION genomic survey sequence.
ACCESSION BZ993822
VERSION BZ993822.1 GI:29237239
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 764)
Whiteley, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Bennezen, J., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFJ230TB
Contact: Cathy Whiteley

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteley@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source 1 location/Qualifiers
1 764
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA360F12"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPo; Site: 1; EcorI; 0.6-1.0 kb high
Cot selected genomic DNA library"

Alignment Scores:
Pred. No.: 9.15e+03 Length: 764
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BZ993822 (1-764)

OY 1 SerleuileThrTPanille 7
Db 655 TCACTGATCACCCTGGAATGTA 675

RESULT 194
CA327827
LOCUS CA327827 767 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FPO-ccw-b-15-0-UI.r1 NIH BMAP_FPO Mus musculus cDNA clone
IMAGE:6825232 5', mRNA sequence.
ACCESSION CA327827
VERSION CA327827.1 GI:24545925
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 767)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5.
FEATURES
source
Location/Qualifiers
1..767
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6825232"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP FPO"
/note="Organ: Brain; Vector: PYX-Asc; Site 1: Bcor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Bcor I adaptor, digested with NotI and then cloned
directionally into PYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN
Alignment Scores:
Pred. No.: 9.19e+03 Length: 767
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CA327827 (1-767)
QY 1 SerLeuIleThrTTPaenIle 7
DB 36 TCTTTGGTCACATGGAACATA 16
RESULT 195

BUT58712
LOCUS BUT58712 769 bp mRNA linear EST 10-OCT-2002
DEFINITION UI-R-FPO-coy-g-20-0-UI.s1 NCI CGAP_FPO Rattus norvegicus cDNA clone
UI-R-FPO-coy-g-20-0-UI 3', mRNA sequence.
ACCESSION BUT58712
VERSION BUT58712.1 GI:23721519
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 769)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
Tissue Procurement: Jeff Stevens, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: DISTRIBUTION: Researchers may obtain clones
from Research Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
source
Location/Qualifiers
1..769
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="UI-R-FPO-coy-g-20-0-UI"
/tissue_type="Mixed tissues"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1ib="NCI CGAP_FPO"
/note="Vector: pT73-Pac (Pharmacia) with a modified
polylinker; Site 1: Bcor I; Site 2: Not I; UI-R-FPO is a
subtracted cDNA library containing the following
tissue(s): Normal cartilage and SR-JWS tumor line. The
subtraction was made according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for these libraries are: CTAATGACG,
CATCTTCTGA,
TAG_TISSUE-rat SRC-JWS tumor line
TAG_LIB=UI-R-FPO
TAG_SEQ=CATTCTTCTGA"

ORIGIN
Alignment Scores:
Pred. No.: 9.22e+03 Length: 769
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BUT58712 (1-769)
QY 1 SerLeuIleThrTTPaenIle 7
DB 631 TCTTTGGTCACATGGAACATA 651

RESULT 196
BI158794/c 779 bp mRNA linear EST 05-JUL-2001
LOCUS 60292158791 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5062076 5',
DEFINITION mRNA sequence.
ACCESSION BI158794
VERSION BI158794.1 GI:14618795
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 779)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1M1167 row: m column: 21
High quality sequence stop: 634.
Location/Qualifiers
1..779
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5062076"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_idb="NCI CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
ORIGIN
Alignment Scores:
Pred. No.: 9.36e+03 Length: 779
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 2 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BI158794 (1-779)
QY 1 SerLeuileThrtTpAnille 7
DB 491 TCTTGTGTCACATGGAACATA 471
RESULT 197
CA327598 781 bp mRNA linear EST 09-JUL-2003
LOCUS CA327598/c 781 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FY0-ccz-d-23-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE:6826440 5', mRNA sequence.
ACCESSION CA327598
VERSION CA327598.1 GI:24545696
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 781)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1..781
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6826440"
/tissue_type="whole brain"
/dev_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"
/lab_host="DH10B (11 bpase resistant)"
/clone_idb="NIH BMAP FY0"
/note="Organ: Brain; Vector: pYX-Acc; Site 1: EcoR I;
Site 2: Not I. The library was constructed according
to Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to NMP. Double strand cDNA was
directionally ligated into pYX-Acc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACAC. This library was created for the University
Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Hainin Chin, Ph.D.,
program coordinator."
ORIGIN
Alignment Scores:
Pred. No.: 9.39e+03 Length: 781
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 6 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CA327598 (1-781)
QY 1 SerLeuileThrtTpAnille 7
DB 536 TCTTGTGTCACATGGAACATA 516
RESULT 198
CX780657/c 785 bp mRNA linear EST 23-FEB-2004
LOCUS CX780657/c 785 bp mRNA linear EST 23-FEB-2004
DEFINITION UI-M-HD0-cko-b-24-0-UI.r1 NIH_BMAP_HD0 Mus musculus cDNA clone
IMAGE:30615199 5', mRNA sequence.
ACCESSION CX780657
VERSION CX780657.1 GI:42746335
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 785)

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES

source

Seq primer: pYX-5
Location/Qualifiers
1..785
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30613199"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH BMAP HD0"
/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTAATGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Alignment Scores:
Pred. No.: 9.45e+03 Length: 785
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CK780657 (1-785)

QY 1 SerLeu11eThrTPsantle 7
|||||:|||||
DB 230 TCTTTGTCACATGGAACATA 270

RESULT 199

CA505075/C

LOCUS UI-R-FU0-cpy-1-21-0-UI-s1 UI-R-FU0 Rattus norvegicus cDNA clone
DEFINITION UI-R-FU0-cpy-1-21-0-UI 3', mRNA sequence.
ACCESSION CA505075
VERSION CA505075.1 GI:24996029
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 797)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
AUTHORS Normalization and subtraction: two approaches to facilitate gene
TITLE discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED

COMMENT

8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 101-157, >(CA)n\$imple_repeat
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

source

Location/Qualifiers
1..797
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-FU0-cpy-1-21-0-UI"
/tissue_type="embryo"
/dev_stage="embryo"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1lb="UI-R-FU0"
/note="Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I;
UI-R-FU0 is a cDNA library containing the following
tissue(s): rat embryo. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pYX-Asc
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CATCTCTACT. This library
was created for the University of Iowa Program for Rat
Gene Discovery and Mapping (Val Sheffield, Bento Soares
and Tom Casavant)
TAG_TISSUE=rat-embryo
TAG_L1B=UI-R-FU0
TAG_SEQ=CATCTCTACT"

ORIGIN

Alignment Scores:
Pred. No.: 9.62e+03 Length: 797
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CA505075 (1-797)

QY 1 SerLeu11eThrTPsantle 7
|||||:|||||
DB 614 TCTTTGTCACATGGAACATA 594

RESULT 200

CG455947/C

LOCUS CG455947 803 bp DNA linear GSS 17-SEP-2003
DEFINITION PUPXF86TB.1_ZM 0.6 1.0 KB Zee mays genomic clone ZMBRna0753p04,
genomic survey sequence.
ACCESSION CG455947
VERSION CG455947.1 GI:34840947
KEYWORDS GSS.
SOURCE Zee mays
ORGANISM Zee mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 803)

REFERENCE

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Benneken, J.

AUTHORS

TITLE

JOURNAL

COMMENT

Maize Genomics Consortium
Unpublished (2003)
Other GSAs: PUFKPF86TBP PUFKPF86TDB
Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

FEATURES

source

Location/Qualifiers
1..803
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA0753P04"
/clone_lib="ZM 0.6-1.0 KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Alignment Scores:

Prod. No.: 9.71e+03 length: 803
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 10 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CG455947 (1-803)

Oy 1 Serleu1ethrTpaanlle 7

Db 601 TCACATCCTCCTGCAATGTA 581

Search completed: March 16, 2006, 04:55:47
Job time : 616.738 secs